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<b>(54) Title:</b> BIALLELIC MARKERS  <b>(57) Abstract</b>  The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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## BIALLELIC MARKERS

## RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996,  
5 the entire teachings of which are incorporated herein by reference.

## BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution,  
10 generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and  
15 is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In  
20 many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism  
25 (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., W0 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include  $\beta$ -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater



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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a

5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays

10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for

15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to

20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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## SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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## DETAILED DESCRIPTION OF THE INVENTION

## DEFINITIONS

- An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.
- Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.
- Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).
- As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

#### I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference  
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being  
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table  
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the  
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are  
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

## II. Analysis of Polymorphisms

### A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid  
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988), transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

### B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,



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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

#### 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

## 2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

### 3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in  
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows  
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of  
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

### 4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of  
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,  
30 1988)).

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## 5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

## 10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

## 25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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## A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See  
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in  
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with - polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population  
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic  
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of  
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime  
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(\text{ID})$  is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies  $x$  and  $y$ , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote:  $p(\text{AA}) = x^2$   
 Homozygote:  $p(\text{BB}) = y^2 = (1-x)^2$   
 Single Heterozygote:  $p(\text{AB}) = p(\text{BA}) = xy = x(1-x)$   
 Both Heterozygotes:  $p(\text{AB}+\text{BA}) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e, the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(\text{ID}) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity  $p(\text{ID})$  for a 3-allele system where the alleles have the frequencies in the population of  $x$ ,  $y$  and  $z$ , respectively, is equal to the sum of the squares of the genotype frequencies:

25 
$$p(\text{ID}) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of  $n$  alleles, the appropriate binomial expansion is used to calculate  $p(\text{ID})$  and  $p(\text{exc})$ .

The cumulative probability of identity ( $\text{cum } p(\text{ID})$ ) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30 
$$\text{cum } p(\text{ID}) = p(\text{ID1})p(\text{ID2})p(\text{ID3}) \dots p(\text{IDn})$$

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The cumulative probability of non-identity for  $n$  loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5        If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10        B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15        Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20        If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child  
25        attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30        The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site  $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$ ), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

### C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the



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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of  
5 individuals who have been tested for the presence or  
absence of a phenotypic trait of interest and for  
polymorphic markers sets. To perform such analysis, the  
presence or absence of a set of polymorphisms (i.e. a  
polymorphic set) is determined for a set of the  
10 individuals, some of whom exhibit a particular trait, and  
some of which exhibit lack of the trait. The alleles of  
each polymorphism of the set are then reviewed to determine  
whether the presence or absence of a particular allele is  
associated with the trait of interest. Correlation can be  
15 performed by standard statistical methods such as a  $\kappa$ -  
squared test and statistically significant correlations  
between polymorphic form(s) and phenotypic characteristics  
are noted. For example, it might be found that the  
presence of allele A1 at polymorphism A correlates with  
20 heart disease. As a further example, it might be found  
that the combined presence of allele A1 at polymorphism A  
and allele B1 at polymorphism B correlates with increased  
milk production of a farm animal.

Such correlations can be exploited in several ways. In  
25 the case of a strong correlation between a set of one or  
more polymorphic forms and a disease for which treatment is  
available, detection of the polymorphic form set in a human  
or animal patient may justify immediate administration of  
treatment, or at least the institution of regular  
30 monitoring of the patient. Detection of a polymorphic form  
correlated with serious disease in a couple contemplating a  
family may also be valuable to the couple in their  
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where  $Y_{ijkpn}$  is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record;  $\mu$  is an overall mean;  $YS_i$  is the effect common to all cows calving in year $_i$  season;  $X_k$  is the effect common to cows in either the high or average selection line;  $\beta_1$  to  $\beta_{17}$  are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms;  $PE_n$  is permanent environmental effect common to all records of cow  $n$ ;  $a_n$  is effect of animal  $n$  and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and  $e_p$  is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

#### D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the

10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction  $\theta$ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &

15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions ( $\theta$ ),

20 ranging from  $\theta = 0.0$  (coincident loci) to  $\theta = 0.50$  (unlinked). Thus, the likelihood at a given value of  $\theta$  is: probability of data if loci linked at  $\theta$  to probability of data if loci unlinked. The computed likelihoods are usually expressed as the  $\log_{10}$  of this ratio (i.e., a lod

25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod

30 scores for differing values of  $\theta$  (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of  $\theta$  at which the lod score is the highest is considered to be the best estimate  
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of  $\theta$ ) than the possibility that the two loci are unlinked. By convention, a combined lod  
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.  
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

#### IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some  
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)  
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example *trp*, *lac*, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby,  
5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is  
10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene  
15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating  
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292  
25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate



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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and  
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to  
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*  
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of  
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

#### V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific  
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means  
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

#### 15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to  
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference  
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and  
5 individually indicated to be so incorporated by reference.

[illegible]

WI-9651b	105 A T ---	---	TCTCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCCTCCTCGGAATTCCTTTCCCT ACCTTGCTCCTCATGTACAAATTTCTGCTGCTCCTTCAATGGGGCAGCTTGAAGCCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATCCACTGCCAGGACCCCTTAGGCCCTCTG TCTTTAAACCTGTAAATGGTATATTAAATCCTTGGTGTTTGAATGCTCTC
WI-9651	139 T C ---	---	TCTCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCCTCCTCGGAATTCCTTTCCCT ACCTTGCTCCTCATGTACAAATTTCTGCTGCTCCTTCAAGGGCAGCTTGAAGCCCTCCCTTTAGACACCT CTT/CACAGGTACAGCCGACCATGCCCTACCTCCATGCCACTGCCAGGGACCCCTTAGGCCCTCTGT CTTTAAACCTGTAAATGGTATATTAAATCCTTGGTGTTTGAATGCTCTC
WI-7676b	309 A C ---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTCTTAATCTCTCCACTGATGCATCCTCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGGCTCTCTTGGTGCCTGCTGGGTTGCAGGGGCAGGAAGCGTGTGACTGCAGCTTCTGCTGGTGC TCCCCCGTCTCCTCGGAGGCAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTCTTAATCTCTCCACTGATGCATCCTCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GC/CJGGCTTCTCTTGGTGCCTGCTGGGTTGCAGGGGCAGGAAGCGTGTGACTGCAGCTTCTGCTG GTGCTCCCCCGTCTCCTCGGAGGCAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	CATTATCTTGTCTTGGGCTGTTCATTACCTTCTCTCTCCAAATGAAGAGGATATTTAAGCATCAT CATCTGGCCCTTTTGTAGTTTGAATATTTTGTG[A]TGACTCCTATGCACATGATAAATTTGTTA TGCTTGCTCTTATCTTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTTATGAGGAGAAAGGGA TCACCCCTTTTGGCCTCTACAACCTTATAGATATTTAAATATCTTTT
WI-9986	42 T C ---	---	TTGGTGTGAACCTCAGAAATATAGGGAAATTAAGACAATTTGAAT/A,CJGTACCCCGAGGAACAAGAG CCCTGCACCTGACTCCAAAGGAGTTCTATTTCTGGCTGTTCCAGACTTTTATGATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGATCCAGGGTAGTACTACAAGAACATGTCA ATATCAATAGCATGCATATGGGTTGTGGATTCTTAGAACTTATTGCAATT
WI-7041	174 C A ---	---	GTCTATTGCAGGAGAAACGTCCCTTGCCACTCCCACTCTCATCAGGCCAAGTGGAGACTGGCCAGA GGCCCTGCACATGCAAACTCCAGTCCCTGCCTTCAGAGAGCTGAAAGGGTCCCTCGGCTCTTTATTT CAGGGCTTTGCATGCGCTCTATTCCTCTGCTGCTC[C]A/CACCTCTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAACAAGCTCATTTGTACAGTGTCTGTTCATGTAATAA
WI-7224	134 T C ---	---	ATAAACCTTGTGTATGTATCACCCCACTCACTAATTAATCAACTTAATGCTATCAGATATCCTCTCT ACCTTCACGTTATTTGAAGAAATCCTTAACATCAAAATCTTTTCATCCATAAAATGTCAGCATTT /CJATTAATAAACCAATAACTTTTAAAGAAACATAAGGACACATTTTCAAAATTAATAAAAAATAAG GCATTTAAGGATGGCCTGTGATTATCTTGGGAAGCAGAGTGATTCATGCTAG

WI-10826	132 A C ---	---	TCTATTTCGATTCACAGTAGCCCCCATGAAGTAGGTATAACCCAGCCTCTATTTTAAACATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTCCCTAATAAGCAAAGACCTGCAJWC JCCCTGGCTTCTGACTCCAAAGCTTATCCCTTCTCATGCTGTTGCTGCAGCCAGGAOCCCATGCGCA GAAAGCCAGCCTCTCCATCCCCAC
TIGR- A004S25	145 G A ---	---	AGATCGCCATTAGTATTATTCCTTTGAAGATACITTTGGAGATTCAITTTCTTGAGTGGCACTGCAT GCTCATTGAGTGAAGAACTTTGGGGTATAGAAATGGAATGGAGAGTTTCAACACAGCTTTGCTGAAAC TGACTTTGGGAGCTCCAGACTTCACCTGCTTGGCAATGAAACCATCACCTGGTTTGCACTTCTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24 A T ---	---	AAACACACAGAATCATCAAGCACJATJATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAGTAACCTCGAAATAGTAGGATAGTATTATCAITTTCTGTAATAGATTCACCTCTCAGCAAT TGGTCTGTTTTCATTCTATGGAACCTCTCCGTACTGTAAATTTTCATTCTATGGAACTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121 G T ---	---	TAGTATGCTACTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACITTTGAATGGTCTTGTC TTTCAATAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGGCACTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAAACCAAGAGAAAGAAAACTTGAT
WI-4719b	107 T G ---	---	TTCAITTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTGGGTGTGAGCGGATT ATGCTGACGCCATGGGTTCATAAGTGACTTTGAGAGTTGAGAGTTGAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGATTCATTCAACAATTCGTCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---	---	TTCAITTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTGGGTGTGAGCGGATT AT[G/A]TCGACGCCATGGGTTCATAAGTGACTTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGATTCATTCAACAATTCGTCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---	---	TCAACACGCTTTTATGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTCTTACCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTGTGAGAGGGAGGCCAGACAGGGAGGAATTCAGGGGCATGTATGGCTC AGTCCCACTTCTGCTGCTGCAGAGTATAGGGACCAGGGTTCCAACTTT
WI-9484	178 G A ---	---	TCAACACGCTTTTATGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTCTTACCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTGTGAGAGGGAGGGGCCAGACAGGG[G/A]AGGAATTCAGGGCATGTATG GCTCAGTCCCACCTTCTGACTGCAGAGTATAGGGACCAGGGTTCCAACTTT



WI-7330	207	C T	---	---	AGGATGGAAGGAGACACGGGCGAGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAAATTTCTCTTTAAATGTGGCATATAGGTTT GTGACACAAGAAAGTCATCTTTGGTGGCTAAGTTTACTAAGGAAAAATAACTGAAAGATTAAAG TGAGAG[C/T]TGAAGAAGAGAAATGATAATGCTTCCAACCTGTAGCTGTACAG
WI-9443	211	G A	---	---	TTAAAAACAGTTCAGGTTGGTGAAGCAGAAAAAGGGATGTGATTACAAATTTAAATGAATCAGTCACATT GCACAATTAATCCTTTGGCATCATACAACTGGGTTTAAATGGCAAAATGATGACATCATAGCATGA CCAACACTCATGGAAGGCAGTCTAGAGTCCATCACGCTCACACCTGAGGGGAAGGCACTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCCACATGCCCACTT
WI-7166	59	C T	---	---	TCTCTAAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGGAT CATCAACAAGATTTCCTTTGTGCAAAATATTTGACTATTCTGATCTCTTCATCTCTGACTAAATTCGTG ATTTTCAAGCAGCATCTTCTGGTTTAACTTTGCTGTGAACAATTTGCGAAAAAGAGTCTTCCAAT TAATGCTTTTTATATCTAGGCTACCTGTGGTTAGATTCAAGGCCCGAG
WI-7259b	189	T C	---	---	GCTTCTCCCGAAGCGGGGCTTGGCCTGGAACCTTCAGAGAGGAGCGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCCCTGC AACAGCTGCAGGCTGCTTCTCTCTCTGAGTTCCCTCTGGGCT GCGCAGGCTCCCCGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[T/C]TGGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTTGAGGGGCCCAACTTCCCTTGGAGCTC
WI-7259	188	G T	---	---	GCTTCTCCCGAAGCGGGGCTTGGCCTGGAACCTTCAGAGAGGAGCGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCCCTGC AACAGCTGCAGGCTGCTTCTCTCTCTGAGTTCCCTCTGGGCT GCGCAGGCTCCCCGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[G/C, T]TGGGGGAGCA GAGCCAGCAGGTGGACAGGTGTTTGAGGGGCCCAACTTCCCTTGGAGC
WI-7322	275	A G	---	---	GTACTTTAGGCCTGTGAGGTGGGCAATTTAGTGTGACCTTGACACCGGGTTTCTAACAGATGAC CCTGTGAATCATAAATTTAAACCTGCATATATTTATAGCCAGTCATCTTGCCCTCTCACCCCTATATG GCCATAAACTGCCTAAGCACTCAGGCCCTCCCACTCATCAACCCCTTTGACCAGAGAAAGCACTC TGGTTCTCTATCCCTTGTACATAGAGAGTTTGTCATGGGGCCTCTGGCTG
WI-7685	46	T C	---	---	TCAGTTCTAGTCTCTGCGGGCCACACAGAAACCTTTTTGGGCTCT[C/T]TTTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAGGCTTGGAGCTGAGCCCTCTCACCTGTACTCTTCGGAATAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCCTCTCCCTCTGCGGACTC CTGGGTTGAGCTGTGCTCAGTCCCTCCCAACAGATGCTTTCTGTCTC
WI-563	87	G A	---	---	TGTGACCAATTGTTATTTTAGAGGGTTTAACAATGGCTGACTATCACCTGATGGTGCAGAAATTC CTGGGGGAGGCTCCCCCT[G/A]CCCTGATCATGCTACCTAAGCTGCTACTCTAACAATACTACTCC TGTGTATGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGCAGAT

WI-931c	191	C A ---	---	GACCAGGGACACGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTCTGCTGTGTCAAAATGATCCTTCT GTTGCTGCACTGTCACTTACTGTTGTATGGATTATAATTATGTCCAAAAAGCC[C/A]GAGGCTGG TACAGAAAGGCATGGGAAAGATGTGTGAGA
WI-931b	81	A G ---	---	GACCAGGGACACGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTA/GJCCCTCACCACACCTTCCAGTGTCTTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCACTTACTGTTGTATGGATTATAATTATGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTGAGA
WI-931	31	A G ---	---	GACCAGGGACACGAAAGCCACGGAAGCCAC/GJGCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCACTTACTGTTGTATGGATTATAATTATGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTGAGA
WI-10870b	91	C T ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATACAAGAAATCTTGGGACCTGTACTCTCTGATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCCC
WI-10870	103	G A ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGACACCTACTTAGA/G/AJGAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATACAAGAAATCTTGGGACCTGTACTCTCTGATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCCC
WI-7719b	281	T C ---	---	AGTTTATCTTCCAGATGACGAGTAGACAAATGGATACTAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCTCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163	A G ---	---	AGTTTATCTTCCAGATGACGAGTAGACAAATGGATACTAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC/GJTTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCTCTCACTGATGATTTCAAGCTAAA
WI-10396	72	C A ---	---	GCCTTGGAGTATATCTAAACTGTGGCCTCCACTTTCATTTTCTTGAACATGCTATCAACTGGGAA GAGT[C/A]GTGACTTTATGCCCAGTTCCCTCTCAGATTTTATGACGGTTGTTTTCTTTTGTTA TGCCATTTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCTCCATTGCTGTCAGG TTAACAGCCACCATTTGTAAACACTTTGT

WI-10673	94 C G ---			TCCCTTTATGACCCCAAGAGATATTATTAAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCGGTGGCACTCATGGAGGGG[C/G]TCAGGTTGAACTATGCAGTGTGCTCCGGCCACACA TCCTGCTGGCCCTACCTGCCCAATTCATCTCCCAATTAATCTGCTTATTGTTTCATCCTG GAGAAITGAAGGGAGGTCAGTTGTTGTCATGATTGTCAGAGAACCT
WI-7842	57 T C ---			CACAGCCATGCCCTTGAGGAGCCGCCACAGATGCTGAATCCCTATCCCATCTGTC/GJATGAG TCCCAITTCCTTGCAATTAGCAATCTGCTCCCCCAAAAGAAATGCTATGAAGCTTTCTTCCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGTCTTAGTACCAGAGCTAGTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAGCAATGATTCAGCTCCCTTATA
WI-7721	145 A C ---			CTGCCTCATCAGCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGGCTGCCATGCTCTGG AGGAGCAAGGGGGCCACATCCCCACCCAGCTGTACCCAGCCGGGCGAGTGACGCCCTTCCTCCG TGCTCTGC/CJCTGACTCTCTTTGAGGTCCTGTATGCTACCTCTGACTCTGCTGGTCCCTCTG TGCTGCTCTCATCCATCCTCTTACTGGGGCTGGGGCTCTAGCCCAA
WI-4767b	173 C A ---			TTTCCAGTCTGTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGA/C/GJATTCATAAAGAGTT CAGGTCCTGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTGGAGAGGGTATGTT CTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACA/C/AJAACTCACTAAGGAATCCACTAAGA CTCCTCTAACCCAGAGATTTTAACT
WI-4767	50 A G ---			TTTCCAGTCTGTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGA/C/GJATTCATAAAGAGTT CCTCAGGTCGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTGGAGAGGGTATG TTTCTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATCCACTAAGAC TCCTCTAACCCAGAGATTTTAACT
WI-7718f	222 C T ---			ATTGCACTGAAGTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAGTG ACTTTGCAGATGGAAAGAGGTGAAATGAAGAGGAGCTGTGTTGAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA/C/TJCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718e	60 T C ---			ATTGCACTGAAGTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGA/T/C]GCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718d	31 G A ---			ATTGCACTGAAGTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGA/TGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	91	C G	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCCGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAATGAAGAAAGGAGCTGTGTTGAACACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718b	248	A G	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGAGATAGATG ACTTTGCAGATGGAAAGAGGTGAAATGAAGAAAGGAGCTGTGTTGAACACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATT[A/G]AT
WI-7718a	42	A T	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGC[W/C.T]GTTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGAGAT AGATGACTTTGCAGATGGAAAGAGGTGAAATGAAGAAAGGAGCTGTGTTGAACACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATT
WI-7227d	99	G C	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC CGTGACCAATTATCTTTAGACAAGCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291	G A	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC CGTGACCAATTATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT GGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACAGTG TTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93	G T	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC CGTGACCAATTATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24	A G	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC TTCCGTGGACCAATTATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234	A C	---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGCTCTGGAGGTGGGAGACAAGAACCTCCG AAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATGCTTTCATCGAACAACTGATCGGAAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACCTGAGCCAAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA[AC]ATGATCTTGAGATTTC

WI-7310a	64	T A ---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGTCTGGAGGTGGGAGACAAGGAACCTT/A JCCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTGTGATCTTCATCGAACAACTGATCGGAA AATTTGAATCTGTTACTGAAATGAGGAGAGAGACATGTGCTATTGAACAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCTCCATCCCAATGATCTTGAGATTTC
WI-7878b	162	A G ---	---	CCAGCAACACCTACACCTTGTACCTGCTGGACTCCTATGATGGCTGCTGGTTGATAATAATCA GATCATGCCAAGACGGGCTCCTGATAATCGTCTGGCATGATTGCAATGGAGGGCAAAATGCGTCC CTGAGGAGAAATCTGGGAGGAGCTG/GGTGTGATGAAGGTGTATGTTGGGAGGAGCACAGTGT CTGTGGGAGCCAGGAAGCTGTCAACCAAGATTGGTGCAGGAAACTA
WI-7878a	51	C G ---	---	CCAGCAACACCTACACCTTGTACCTGCTGGACTCCTATGATGGCTG/C/GTGGTTGATAATAA TCAGATCATGCCAAGACGGGCTCCTGATAATCGTCTGGCATGATTGCAATGGAGGGCAAAATGC GTCCCTGAGGAGAAATCTGGGAGGAGCTGATGATGAAGGTGTATGTTGGGAGGAGCACAGTG TCGTGGGAGCCAGGAAGCTGTCAACCAAGATTGGTGCAGGAAACTA
WI-7381c	213	C T ---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTTCTACC AGCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTCTGCTATGGTGAGATC AGATGTGCCAAGGAAGGAGCTCTGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAGACA AAACGGCTC/C/TGGCTCTCAGAGCATAATCCTTGGCAGGCTCAGCAGG
WI-7381b	54	C G ---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCC/C/G/CCTTTCTTTCT ACCAGCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTCTGCTATGGTGAG ATCAGATGTGCCAAGGAAGGAGCTCTGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGCTCAGCAGG
WI-7381a	53	C G ---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCC/C/G/CCTTTCTTTCT ACCAGCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTCTGCTATGGTGAG ATCAGATGTGCCAAGGAAGGAGCTCTGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGCTCAGCAGG
WI-1017b	93	G A ---	---	AAATTGCTCTATTCCGACCTCATATTAAATAGAGCAATGAGAGCGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGACCAAGAG/GA/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTCCCATTTTACAAATAAGGAGACAAAAATAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGAGGTTTGTCCC
WI-1017a	92	G A ---	---	AAATTGCTCTATTCCGACCTCATATTAAATAGAGCAATGAGAGCGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGACCAAGAG/GA/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTCCCATTTTACAAATAAGGAGACAAAAATAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGAGGTTTGTCCC

WI-1795b	130 T C ---	---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCGGGTTCTCCAGACTCCTACGATTA AATTGTATGCATGTGAACAACCTGATGAGGTACTTAGATCTCAGTGTCTTGCAGAAAGAAAGTTC/C GTCTACCAATTTTACCAAATTCGTAGTACAAATTAAGTATCTCTTGTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGAGGATTT
WI-1795a	47 T C ---	---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCGGGTTTC/CCTCCAGACTCCTACGA TTAAATGTATGCATGTGAACAACCTGATGAGGTACTTAGATCTCAGTGTCTTGCAGAAAGAAAGTCTC GTCTACCAATTTTACCAAATTCGTAGTACAAATTAAGTATCTCTTGTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGAGGATTT
WI-10616d	136 G A ---	---	---	CACACAATTTGCAAAACACTTCAAAAGTGAACGCCCGACATCATAGCCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCCTATCACATTGCCA C/GA/TAGCCCTCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616c	136 G A ---	---	---	CACACAATTTGCAAAACACTTCAAAAGTGAACGCCCGACATCATAGCCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCCTATCACATTGCCA C/GA/TAGCCCTCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616b	141 C T ---	---	---	CACACAATTTGCAAAACACTTCAAAAGTGAACGCCCGACATCATAGCCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCCTATCACATTGCCA CGTAGC/C/TCTCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616a	116 G C ---	---	---	CACACAATTTGCAAAACACTTCAAAAGTGAACGCCCGACATCATAGCCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCCTATCACATTGCCA CCAGTAGCCCTCCCTTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-1126c	52 G A ---	---	---	CTCTTATTTCTCTGGGCACCTGCTTTCTTTGGGGCAAACTTCCAGTATCAGTATCACTG/AJATACTAATAA AAACCCGTGAAGTCTGCTTGCAATTTTCAAGATTCAATATATATATATCCAGATTGTTTCCCGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATATTTAATTTTCAGTTTCTCAAAAGGAATATGAAATTT TGTTAAATGCAATCCAGCTGTAACTTTTGGACTTGCTTTATTTCTT
WI-1126b	230 T C ---	---	---	CTCTTATTTCTCTGGGCACCTGCTTTCTTTGGGGCAAACTTCCAGTATCAGTATCACTAATAATAA CCCTGTAAGTCTGCTTGCAATTTTCAAGATTCAATATATATATATATCCAGATTGTTTCCCGCAAGAAATTT TTATTTCTCAAGATATAAAAAATAAATATTTAATTTTCAGTTTCTCAAAAGGAATATGAAATTTGTT AAAAATGCAATCCAGCTGTAACTTTTTC/C/GGACTTGCTTTATTTCTT

WI-1126a	97	T C ---	CTCTATTCTCTGGGCACTGCTTTCTTTGGGGGCAAACTTCCAGTATCACTGATACACTACTAATAATAAAAA CCCTGTAAGTCTGCTTGCAATTTTCAAGATT[C]CAATATATATCCAGATGTTTTTCCCAGCAAGAAAA ATTTTATTCTCAAGATATAAAAAATAAATAATTTAAATTTTCACTTCCCTCAAAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAAC:TTTTTTGGACTTGCTTTTATTCTT
WI-11183c	124	C T ---	TAGTGCTAAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTTTGCCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGATGATAGAGTTTTAAATATTTGGT ATGTTGGTCTAGAGTTAGTAATGGAA
WI-11183b	192	T C ---	TAGTGCTAAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTTTGCCCTTGTCACATAACATTT ATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGATGATAGAGTTTTAAAT[C]ATTGGT ATGTTGGTCTAGAGTTAGTAATGGAA
WI-11183a	118	C T ---	TAGTGCTAAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTTTGCCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGATGATAGAGTTTTAAATATTGGT ATGTTGGTCTAGAGTTAGTAATGGAA
WI-10770b	174	G A ---	GCTTGGTTGCTTTAGTCTTATTGTCTCAGCTTGGCTGCTCCCTTTCTGCTGGCCCTTTTGATTTCA CCCATACCTCTATGCCCTCGTCTCAGACCATTTCCCTCTATCTGGAGCGCTCTCCCTGTACTTTCTCTG TTCACCAACCTTCTTTTATCTTCAGGACACTCA[G]ATTACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGTGTCCTTTCC
WI-10770a	49	G T ---	GATGACAACTTCTGCTGTGACCCCTTAGTCTTGTCTCATGACACTTTTCAATCTCTGCCCTGTATCATGG TTATCACTGGACA[C]TAGCCACCTCCCCAGAGGCTTAGAACCTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAAATTCGCAATCT
WI-9667b	82	C T ---	GATGACAACTTCTGCTGTGACCCCTTAGTCTTGTCTCATGACACTTTTCAATCTCTGCCCTGTATCATG GCTTATCACTGGACAGACGACCTCCCCAGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAAATTCGCAATCT
WI-9667a	68	G C ---	GATGACAACTTCTGCTGTGACCCCTTAGTCTTGTCTCATGACACTTTTCAATCTCTGCCCTGTATCATG GCTTATCACTGGACAGACGACCTCCCCAGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAAATTCGCAATCT

WI-10400d	189 A G ---	---	ACATTTATTAGCAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATAATTTATTCTAATTT TCITTCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTC/A/GJTGCCATGTAG TTTTTGGTTTCATTTACTTGCAAAATTTCAAGGGCGTTAATGCATTATG
WI-10400c	166 A C ---	---	ACATTTATTAGCAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATAATTTATTCTAATTT TCITTCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTTCATTTACTTGCAAAATTTCAAGGGCGTTAATGCATTATG
WI-10400b	165 A G ---	---	ACATTTATTAGCAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATAATTTATTCTAATTT TCITTCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTTCATTTACTTGCAAAATTTCAAGGGCGTTAATGCATTATG
WI-10400a	46 T C ---	---	ACATTTATTAGCAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTAGACATCT GCTGGTTAACTGTTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATAATTTATTCTA ATTTTCCTTCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGT AGTTTGTGGTTTCATTTACTTGCAAAATTTCAAGGGCGTTAATGCATTATG
WI-10809b	78 C T ---	---	AAAGGGCTACAAACTAAGGCCAAAAACCATGAACGGTATAAGGAGGTAATGCAAGGGAGACCC CACCTCTACCA/C/TTAGAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATACTGGTTAG CAACAAATGGAATGTATTAGCCCAAGGCAAGGGTATGGACCAAAAGTGCCCAAGTATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---	---	AAAGGGCTACAAACTAAGGCCAAAAACCATGAACGGTATAAGGAGGTAATGCAAGGGAGAGA CCCCACTCTACCACTTAGAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATACTGGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCAAGGGTATGGACCAAAAGTGCCCAAGTATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGAAGACTGTGAGGAAAGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTTGAT CATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140 A C ---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGA/C/GACTGTGAGGAAAGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTT GATCATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTTCTGA



WI-7038a	31	G A ---	---	CGAGCTTGGGATAAGCAAGGGGACCTTGGC[G/A]CTCAGCTTCCCTGCCACAICCCAGCTTGTTG TCCCAATGAATACTGAGATGCTGGGTGCTCTCCCTTCCAGGAATGCTGGCCCCCAGCCTGGCCA GACAAAGAGACTGTCAGGAAGGTGCGAGTCTGTAAACCAGCATAACAGTTTGGCTTTTTCACATT GATCATTTTATATGAATAAAGATCCTGCATTTATGGTGTAGTTCTGA
WI-3429b	64	G T ---	---	ATACGCTTCTGCTGTCCACAGTGAACCAAGCCAGCCAGGTGGCGGCTCCACACA[G/T] CCCTCAGCCCTTCAGCTTTCAGTGTGCTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAAATACAGATCCCAAGTCTCCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTCTAGAA TCCTGACTGTTAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T ---	---	ATACGCTTCTGCTGTCCACAGTGAACCAAGCCAGCCAGGTGGCGGCTCCACACA[C/T]AG CCCTCAGCCCTTCAGCTTTCAGTGTGCTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAAATACAGATCCCAAGTCTCCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTCTAGAA TCCTGACTGTTAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A ---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTGGCGAAAGGATAAAGAAAGTGAGTGACGGTGACCT GTAGCCCCATTCCT[G/A]TGGGATAAGGTGCCATTGTTCTTGGAGGGTGAAAATGCCACATTC TTTTGGCAGGGGACACTCCTCTGGGTGCTCTATTGCTCAGTTTCAICATT
WI-6786b	111	A T ---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTGGCGAAAGGATAAAGAAAGTGAGTGACGGTGGA CCTGTGAGCCCCATTCCTCTGGGATAAGGTGCCATTGTTCTTGGAGGGTGAAAATGCCACATTC TTTTGGCAGGGGACACTCCTCTGGGTGCTCTATTGCTCAGTTTCAICATT
WI-6786a	106	A T ---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTGGCGAAAGTGGATAAAGAAAGTGAGTGACGGTGA CCTGTGAGCCCCATTCCTCTGGGATAAGGTGCCATTGTTCTTGGAGGGTGAAAATGCCACATTC TTTTGGCAGGGGACACTCCTCTGGGTGCTCTATTGCTCAGTTTCAICATT
WI-6711b	226	G T ---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAAATTAATAAGTATTGGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCAACTCACTCTGAAT TTCATATACCTCCATTATTAAATCAATACATCATTCAGAGAAAAGACACGGTGCCAACTGGGTT TGGTTGGTGGCTGCACACCCACAG[G/T]TGGCACTAAGTGTAATCTCTAAA
WI-6711a	36	T C ---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAAATTAATAAGTATTGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCAACTCACTCT GAATTCATATACCTCCATTATTAAATCAATACATCATTCAGAGAAAAGACACGGTGCCAACTG GGTTTGGTGGTGGCTGCACACCCACAGTGCGCAACTAAGTGAATCTCTAAA

WI-10613b	172 A C ---	---	ATTTGATGCCAAAATCATAATACCCCTGCATTCTAGAACATACAGTGAATAGAAATTTTGAGCCATA TGGTGAATAATTTAGAAATTAATTTCTCTATATATACTACGTTTAACATCAATGAATGTGATTT TTTGCAACTTTTGACAGGCCAGGCAATTTTATTG/C/GCCCTAGGAGGTTACTATAATTTAGA AAGGCTTACCTCCACTCTATAATTTAAGTCTCGGACTAGGATGTAG
WI-10613a	44 G A ---	---	ATTTGATGCCAAAATCATAATACCCCTGCATTCTAGAACATACAGTGAATAGAAATTTTGAGCC ATATGGTGAATAATTTAGAAATTAATTTCTCTATATATACTACGTTTAACATCAATGAATGTG ATTTTGTCAACTTTTGACAGGCCAGGCAATTTTATTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTTACCTCCACTCTATAATTTAAGTCTCGGACTAGGATGTAG
WI-7587c	133 A T ---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCCTTGAAGC ACATCCCTTCTGTGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA/W TJGGAATGAACCACTCCCTGCCATTCCTATAAGATATCCCAAGACCCAGGCAATTTTGCCCTCT TTCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587b	81 G A ---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCCTTGAAGC ACATCCCTTCTGTGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCTATAAGATATCCCAAGACCCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587a	28 C T ---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCCTTGAAGC AGCACATCCCTTCTGTGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCTATAAGATATCCCAAGACCCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-10681b	103 T A ---	---	ATGACTCAGGTGACAAAAGAGCATGCTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAAGACATCCTTTTAAAGAGCC/T/AAAGACAGCCATTTTAACTCAATTCG TAGTTTATGATTTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTGGAGAGGAGGTGACGCTCTGTTAAAG
WI-10681a	41 A T ---	---	ATGACTCAGGTGACAAAAGAGCATGCTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCTTTTAAAGAGCCTAAGACAGCCATTTTAACTCAATTCG TAGTTTATGATTTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTGGAGAGGAGGTGACGCTCTGTTAAAG
WI-7222c	126 G T ---	---	GCCTCTCCTCAACTGTCTGGACCCAAAGGCTAGGAAAGGCTGCTTGAGATGACTTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGTCAAGGTGACCCCTGTTCTCAAGTTGGGGATGGG/GTAAATAA AGGAGGGGAATCCCTTGAACAAGAAAGAACTGGGGATGTTATATTCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTGTGTTTCAAGAGACTCGAATTCATTTT

WI-7222b	255	G A ---	---	GCCTCTCTCAACTGTCTGGACCCAGGCTAGGAAGGCTGCTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCACCCCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTCACCTGCCCTTGAAGCTTTAA GACAGTGAATTTTGTGAAGTTGTATTTCAAAGACTCGAATTCATTTCTCA
WI-7222a	126	G T ---	---	GCCTCTCTCAACTGTCTGGACCCAGGCTAGGAAGGCTGCTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCACCCCTGTTCTCAAGTTGGGGATGGG[TAATAA AGGAGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTCACCTGCCCTTGAAGCTT TAAGACAGTGAATTTTGTGAAGTTGTATTTCAAAGACTCGAATTCATTTT
WI-8054d	41	C A ---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTCTCTTTC/AJTATCTCTCCAGTTCAAAATG CTTGCACTCTTTAATAGCCAGCATCTCTTAGATCTGAGTTGGCTCAACGCACTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCCTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTATACAGCGCGCTTCCCTGGCGTACAGAGATCCTTGCCCTT
WI-8054c	237	G T ---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTCTCTTCTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGAGTTGGCTCAACGCACTCAAGCCTTAGCACAA TCTCTTTGTAGTTTAGCCCTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCTTCC TGTATACAGCGCGCTTCCCTGGCGTACAGAGATCCTTGCCCTT
WI-8054b	148	T C ---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTCTCTTCTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGAGTTGGCTCAACGCACTCAAGCCTTAGIC/GJA CAATCTCTTTGTAGTTTAGCCCTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTATACAGCGCGCTTCCCTGGCGTACAGAGATCCTTGCCCTT
WI-8054a	131	C G ---	---	TTCCACAAAACCTTCCCTGGCGGCTGACTAAGATGAGAACTGGGAGAACTGGATAGTTAATAA ATGTTTATATTTTACTTTAAGCGAAGTTGAACACGAGACGATAGTTAACGCTGTTAAGTTTAT ACGGTGTGCGAGGCAACA/GTJGAGAGGTACGGGAATAGTTCTACTCTCTGTTTTTATTCTTG TTTTAGACACAGGCTGCTGTGTG
WI-10854b	152	G T ---	---	TTCCACAAAACCTTCCCTGGCGGCTGACTAAGATGAGAACTGGGAGAACTGGATAGTTAATAA ATGTTTATATTTTACTTTAAGCGAAGTTGAACA/CJTJGAAGACGATAGTTAACGCTGTTAAGTT TATACGGTGTGCGAGGCAACAGGAGAGGTACGGGAATAGTTCTACTCTCTGTTTTTATTCTTG TTTTAGACACAGGCTGCTGTGTG
WI-10854a	102	C T ---	---	TTTTAGACACAGGCTGCTGTGTG

WI-9826b	127	G A ---	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGCCCCACAGGCCCAATTCAGCCATGCCATATTTTGTG TGCCTGATGGCTGTTGGTGTGTTTGACACGAGTTGAGCCATTGTACAGAGGCTGTATG/AGCCTT CAAAGCCAAAAAATAATTTACTCTCGCCCTTGACGGAAAGTTTGCTGATTCTAGATAATTTAAA GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125	A T ---	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGCCCCACAGGCCCAATTCAGCCATGCCATATTTTGTG TGCCTGATGGCTGTTGGTGTGTTTGACACGAGTTGAGCCATTGTACAGAGGCTGTATG/AGCCTT AAAGCCAAAAAATAATTTACTCTCGCCCTTGACGGAAAGTTTGCTGATTCTAGATAATTTAAA GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60	T G G T G G T T T T	T T G T T T G T G T	T G A C A T T A T A T	CGGACACGTGTATACAAATACAGATCGTATGGGTTTGTGTTGTGGGTTTTTTTTTTT/GTTAC ATTTCTTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A G A G	A A C T G C A A A T A G G A A A C C A G	C C A C T G G G G C T C C C	TTCAAGTAACTGCAATAGGAAACCAGAG/AG/AGGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGAGGAGGTGGCCCCCTACACCCITTTAT
WI-8170b	259	G A ---	---	---	GCACTTCTCTCTGAGCAACAGGTACACTTTTTCTCTAACATTGATCTATAACACACCAGAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGTCCTCAAAAGTGAATCCTATCAATCAGAA ATAAAGGTAAAGGGCCCTCAAATGAAATCTACGGAACAAATACACAAAGA
WI-8170a	204	T A ---	---	---	GCACTTCTCTCTGAGCAACAGGTACACTTTTTCTCTAACATTGATCTATAACACACCAGAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGTCCTCAAAAGTGAATCCTATCAATCAGAA A/T/A)AAAGGTAAAGGGCCCTCAAATGAAATCTACGGAACAAATACAC
WI-8172	136	C G G A C A	C C T T A T T A A A A T T G T T T C T T	G A A G A G A A A T G T A A T A C C T G T	CAGGATTCCTTAAGTCATCTCCAAATACCTCCAGGTCAATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACCTCCTTTTATAAAATTTGTTTCTTGACAT A/C/G)AGTACCTTTACAGGTATTACATTTCTCTCACCCTTTACA
WI-8183	56	G A T G C	T G A A A T A A A A A C A A T T C T G T	T G T G T T G A A A T C A A C C T G C	AGCAGGGTTGAAATGATCCCTTATTTACATGAAATAAAAACAATTTCTGTTCG/A)GCAGGTT TGATTTCAACACAGATTGAATCTGTAAAAACCAAGCTCGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83	C T ---	---	---	GCTTTATGGGATTGCAAGGTTACAAGGTTAAAGACAAAACCCCAAGCATGGGATTTTGCCTGAAAT ATTAGCGTTAAAGGAG/C/T)TGAGTTGAGTCAACACAGGGG
WI-8712	44	G A G	C A C A G G G A A G A G G T A G T G G A	C A G G A A G C C T G A C C A T C T C	TCAACAATGACACTGTGTAACAGCACAGGGGAAGAGGTAGTGGAG/G/A)GAGATGGTCAGGCTTCCTG TTCTTAACCCAGAGAGCCCCAGCAACCTAGAGCGCCTCACCTAGCCCTTAAT

WI-8827	22 C T	TCCCTGGGAG C	GGATTAGGAT TTTAGTGTTC	GGTGCCCTGGGAGACTATGG[C]/JAGTGAACACTAAATCCTAATCGCCATGCATTGGAAATTATT CCGACTATTACTTCTTAGTCTCTTCTATCCACCAGCTTCT
WI-8833	51 A T	TCCTCCATGCC ATCTCTG	CCTCACACATT ATAGGGGCA	CTCCGGCCTCTTAAAGCTCTGTAGACTGTCTCTCCATGCCATTCTCTG[A]/JJGCCCTTATAATGT GTGAGGGTATTACATAAGTCCCTATTCAAAGTCCCTTGTCATAAAAGGTACAGCTATGT
WI-8377	63 A G	---	---	ATTTTtagccatgttggtaaaagtTCATTTTcagTACATGGGTAACACCCAGGCCCTTCCC[A]/GJT TATATCCAGTATGCTACAAAGTCTTTTAACTCTTATCAGAAGTATTATTACTGTTTCTTAGAGAG GCTACCAGGCTAAATTCACCTAGTTGGTTGCTAATGTCTCATTATTTATCCTGAAGCTCGTG
WI-8850	21 A G	GGGACTTAAC CTTTGGCCT	CAACACAGCA GGCAGG	GAGGGACTTAACCTTTGGCCT[A]/GJCCTGCCTGGCTGTTGGCTCTGCGCTTGCTGTTTGGTTTCTT TCTCTTACTGGTCTTCTTTGCTTTGCCAGCCACCTATGCTGCTGT
WI-8853	79 C T	CCCGGGCATTG AGGATA	AGTCTTCTGA GCCTTCCAT	ACTTTTCTGAGCTGAGCAACCTCATCTCTTAGCTCTGGTTGATAACGCTGGTTAATCCCGGG CATTGAGGATA[C]/JATGGAAGGCTCAGGAAGACTTCAATCTCAA
WI-8865b	52 A G	---	---	AGGGTGAAGTGAATCACAGGCACAGACTGAGGAAGACAGTCAATGGTGAACAC[A]/GJACAACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTCCATATAAA
WI-8865a	42 T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTGAAGTGAATCACAGGCACAGACTGAGGAAGACAGTCAATGGTGAACACACAAACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTCCATATAAA
WI-8895	32 A C	---	---	GTGCCACAAACCTGGACACCACCAACAGAAAT[A]/CJCTCCGCTCTTGGAAATTTCCATTAAAGAGCA CAATGGGGTAATTATACCAGGGATGCTCCAATCGCTCTTTC
WI-8456	93 G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGGGACTGATATTTTGAAATATAATAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA[G]/JTTATGTCAAGTTAATAAAGATTTCTAAGTCTCACTC TCAACTTCTGTGTTATCTTGCATGGTCCAGTAACAGTTTACACGGCAGACCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCCGTCTGCGTCTCAGTCACCCAC
WI-8496b	157 A G	---	---	TTTTCATCATCAAAAGTTTCTTTCCATAGAAGAAATGGTAATGTTGTATCAGTGCATATTTCTATGGAAA ATTTCATATCTCAAGTAAGTAACTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGGTCA AAGACACAATGCTGCCAATGCA[A]/GJTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41 G A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAAATGGTAATGTTGTATCAGTGCATATTTCTATGG AAAATTTCATATCTCAAGTAAGTAACTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTC TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28 A G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGC[A]/JTCCTCTCTGCGCTTGTACCCACATCCACAGAGCA GOCCTAGTGCCAGGTGCAGCCACTGCCACCCACAGGCAACAGGACCCATGCTGTC

WI-12108	40	C	T	A	T	TGAAAGGG TTAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAAGGGTTAACTCAAATATC[C/T]GAAATACTTTCATTATACCAGGT CAAGAAAATGCCACAGCCAGAAAATTTATTTAA
WI-5989	29	G	A	C	A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAACGTCACAAAGGTCACAGGCA[G/A]CGTACATACGGTTCGTATACCCCATATATTAC CCCTTCATGTCCCTAAAGAAGACATTTCTCTTAGAGATTTTCATTTAGTGTATCTTTAAAAAAAAT CTTGTGTTAACTTGCCTCCATCTTTTCTGGGTGAGGACACC
WI-12201	61	C	T	C	T	CCCTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGCTTTTAGCCTTTTCTGGAGTGTATGTCCCAAGCCCACTGATCACCTGCATG[C/T]GCCA GGTATGGTGGTGGGGTGTGATGGACGTGGTTTCAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31	A	T	T	C	GGCAGCAGC TCTGACTT	GGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAGGACGACGCTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCCCCACATACCA ACTTCTCACCATGATGATTATACCAATAATACAGTTCTTATATAGGGGCTCTGGAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	A	G	C	C	TGGCCTCGCTG CCTC	AGGGATCAAA GAGAAAAGGC	TTTTTCGTTTGTAAATGATCCGAATGCTTGAGAGAAGAAACCTGGCTCGCTGCCTC[A/G]GCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92	A	G	T	T	CATGCCCTTTA AGGATTAAGT	TCTTTTCTCTT TGGTAGTGG	AGCATGTAAGGAGCAGTTTTATTGATTGGTATATTACAGGTTCTAACCCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAGTTTAA[G/CCACACTACCAAAAAGAGAAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T	C	A	T	GTTGAGTATT GTTCTGCTCAT	GGGAAGTCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATTATTCTGATACAACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTGTTCTGCTCATAATTT[C]CCCAATATGTACCAGACCTTCCC
WI-12326	25	G	A	C	A	GACAGACTTC AAAAGCAATT	AGGTTTGAAAA TATGTATTAAAG TACTTTGT	CTGACAGACTTCAAAAGCAATTCAC[G/A]CTTCCAGAATACAAAAGTACTTTAATACATATTTTCAAAC CTGTTTGCAATTTCAAACAAAGTTAGCGTTTGTAAATCAAATTTGATAACCCGACTAAAAAT
WI-12361	63	C	T	---	---	---	---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATATAGGAATTTGAGCATATGTATTAT[C/T] TGAACATAAATTTACAAAAGTGGAAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87	C	T	A	T	CAGACACAGC ATCACACCA	GACCTCCCGT GGC	ATACTGGTTTAAATCCATGTCAAATGTAGTTTACAAAGGGAAGGACAAAGTACCCTTTGTATAGAATAT ACAGACACAGCATCACACCA[C/T]AGGGCCCCACGGGAGGGTGGGGGAGACACACTTTTCCCTGGG AAAGG
WI-11321	67	A	G	T	T	GGGAGGAAAA TCCAATAAAT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTCTGGTGAATCTTTTAAAGCAGGAGGAGGAAAAATCCAAATAAATTTTTTAA A/GJAAGGTTTAGCTATTCCCAATGCTATTTAATACAATGAGGTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11324	40	C	G	T	G	GGATAAATCA TGTCGCCCA	ATCAAGCTTTG GGGCTCT	AGCATACGTCATCTCCTTTATGGATAAATCATGTGCCCA[C/G]AGAGCCCCAAAGCTTGTGATGACAT TCGTAAAGTTACACAAATGTAICTGAAGAAGTTATCTGTTCTGTC

WI-11352a	69	T C G	AGCACAGCAC ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTCCAGAGGAGAGAGATCATCTACATAAGCACACACATAGTGGAA AGT/C/GCTAAGTGCTCCTACGAGAGGTCAGATCATATCCATAGAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTGGAG ATTCTGATTCA	GCCCCGCCCTGA GCAC	TTAGCCCATGCTGTCATTGCAATCACCTGTGAACCTATGAAAACCTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTACAG/C/T/GTGTCTCAGCGGGGCTGGACATCCATGTTTGGGAAGAGTTGGCGCGGT GATTTCGATCGGTATAT
WI-11385	75	T C G T T T	ACAGAAGACT TTCATATTCTT	GATTCATATCT AGTCATGGTCA TATTTT	CTTAAAGCATTATAGTTGGCCTGATGGTGACACAGAGACTTTCATATCTTGTTTTTTAAAGTC TCTTCAGT/C/GAGGAAAAGCTACAGATTTAAAAATATGACCATGACTAGAAATAGAAATCAGC
WI-11388	88	C A A G T T C	TGTTTGAAAT ACACGTAAC	TGCCTTGTATC CAAGTTAAAAT T	TCATGTGCCAGTTAGCTCAGTTGTTAGAGTGTGGAGCTATAAAAAATTAAGAATGAATGTTTG AAATTACACGTAACCTAAGTTC/C/A/TATAATTTTAACTTGGATACAAGGCATTGTTATGCTAAT
WI-11392	55	T G A T A A T A C	GGTATGTGT CTTGAACCTTA	GTACATTCACG TGTTTTGTAAA AAG	TTCATCATTTCCATTAAAAATGGCAGGTTATGTGTCTTGAACCTTAAATAAATAC/T/G/C/T/T/T/TACA AAACACGTGAATGTACTTTCTTGTGAGAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCTTCCCCAGA
WI-11396	52	A T T	TTTTGTTTTG AAATGGTGTTT	AGCTTATTTTC ATATTCACCCA TC	AAAGAAATAGATGGCATTTGTTTCAGTTAATTTTGTGTTTGAATGGTGT/T/AT/GATGGGTGAATA TGAAAATAAGCTTACCTCATCCACTCTAAAGGTAGTTGGTGATTTTGAACCGTTGTCAAT
WI-11441	100	C A C A G C	TCCCCACCAAC CAGC	TGCCAGGGCCT TATTTG	CTGTGAGTCTTTCCCAACTAAACCGTAGTCCAGTATGTCTGGAGGACGCTGTCTGTGTTCTGGTG TATCCCATTAAGTGAATCCCCACCAACCAAGC/C/A/C/AAATAAGGCCCTGGCACAAAAGTAAGCTCTCC ATTTTGTAGAAATGAAT
WI-11466	26	C T T T A T T T T G C A	TGAGAAGCCA TTTATTTTGCA	GTTTATTGTTA TAAAAATGAC CTACAACCT	ACTTTGAGAAGCCCATTTATTTTGCAG/C/T/CTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACCTTCTATTATCTATTATCTCTCACATACATTT CATGTATCCTG
WI-13364	35	A G ---	---	---	TTTTCTTTTGTGCTCTTTTATAGTAGAAGC/A/G/GGGAACAGTTGTCAATACTACTACCTTCTGTGG TCCCCTGTTAGACAACATACCTTTCTTTGAAATGTAAAATGTCA
WI-11276	41	A G A G C A G A C	GGCAGOCAGG AGCAGAC	TGTACTGAGGA GOOGGTG	AGGCAACACTGCTTTATTAGCGCGGAGCCAGGAGCAGAC/A/G/CACCGGCTCCTCAGTACACATT CCCCACCCCTGCCCTGGTCTCCCCACTCAGGGCTGGCATGGAGGGGCGCAGCTAGGTCTGGAA
WI-12210	76	A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTTGC ATAATGTTTTCC	ATTGGAACAACCTTAATAATTGTCATCTCTACATATAGAAAAGCTGCTTTGAATAACTGGGAAAAACA CTATTGCAT/A/G/GGAAAACATATGCAAACTAGCATCAATTGCTCTAGA
WI-14186b	88	A G ---	---	---	AATGGTCTGGTTTTATTGAGAAGCTGTGGTCATTTGATGGAAAGACACATACGGGTACAAAATTACA GGTGGTTTAGTTTACATATG/A/G/TACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT

WI-14186a	52 C T A	GGTCATTGAT GGAAAGACAC	AATAAACCA CCTGTAATTT GTACC	AATGGTCGGTTTATTGAGAAGCTGTTGGTCATTTGATGGAAGACACATAC/C/TJGGTACAAAT ACAGGTGGTTTAGTTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66 A G	GAGAACACTT GTGGGGCTT	GGACCTATCAG TCCATGTTGA	ATTTTGTGGCTATAGGTCAGTGGTTCTAAACCTTGAGCTTGAAGAGAACACTTGTGGGGCTTA/ GTTCAACATGGACTGATAGTCCACCCAGATTCTAACGGTAGGCTGGGGTG
WI-12345	37 C A	GTGGCAGGAA AAAGAGGAA	TTGACAGGGG TTCAGG	GGAAACAGACCTGATCCACGTGGCAGGAAAGAGGAA/C/AJCTGAACCCCTCTGCAAGTATTCTCT TTCTGACCAGCTGGCTTGGCAGCTTGTGAGATTGCAAAA
WI-13416	71 C A	AAATTTTGG AAGTTTTCAG	AGTGTATTAG TTCAATGAATA ATTCAA	GAAAAGGCTGTAATTTTATTTCAAAATTTTGAAGTTTTCAGAAAAAATAAAATGACAAGAACA CATA/C/AJAAATATTGAAATTTATTCATTGAACCTATAACACTTAGCAGAGGAAGGACTTTTGAT
WI-12310	46 G A	TTATCCCAAG TATAATTTA AAAAGC	TGTTTAAATAT GTTGGGTCCT AAA	TTTGAAGAGATGCTGAATTTATCCCAAGTATAATTTTAAAAAGCTJG/AJTTTAGGACCCCAACATA TTTAAACATCTCTACACATACAGAAATTTTCAAGTTTACAAATATCCAGAAGGCAATTTTCTTAAGCAG T
WI-12086	72 C T	CCGGGAAAC TTGGATT	GGAGTCTCGG GTCTGG	GAACCGAGCTTATTGGAGCAAGAGTGTGGACACTGTTTACAACAAAACGTTTCCGGGAAAACCTTG GATTTJ/C/JCCAAGACCCGAGACTCTCCAAGTTCTCACTGTTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102 T G	GGCATAAAGT TCATAATATTC T TTTATG	GGAAAGTCTGT ACAAATCCCC	ATGTCTTCACAGGTTGATTTTGTGAAGAGTTTGTCTATCTAAATTTTCAATTTATTGGCATAAAGT TCATAATATCTTTTATGATCTTTTAAATATCTG/TJ/GGGGATTTGTACAGACTTTTCCCTC
WI-11585	79 T C	TGGTTTGCAA AAACAAA	CCATGCTTCAC TGATACTTCC	TTAGAAGGAAAGAAATAAAACACGGTAATGGGAAATCAGTTCAGAGGTAGGAAGGAGCTGGGTT TGCAAAAACAAAATJ/CJGGAAGTATCAGTGAAGCATGGCCTAGAAATCCAAAGAGCAGGGGTAGAGT TT
WI-11604	68 G C	---	---	TTAGTTGGTTTCCCTGAAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTT/ G/CJAGAACTAGGGACTTTTCCATGAAAATAATTAAGAGCTAAGGAATTTCTGACGCTCACCATTTTTC TTTGTACTCTGCAGTT
WI-11614c	108 C A	---	---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACCTTCACTGTGAAACTGCAAT/C/AJATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60 A G	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAAAATCCAGAAAGACTCAGCTGCTTGJG/JGG CATGTTCCACCCCTGGACTTGCCAACCTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83 T C	---	---	TTGATTTTACTAAGGCTTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACCTCAG ATATTTTAAAAATAAAJ/CJACTTAATAAAGAAATTAGCCATACCACATTTGTTCCATTTGCTAC AAGAACAAAATTGGCAATGA



WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGCTCTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTACAGGATAATATACT CAGATATTTTAAATAAAATTAACCTTAATAATAAGAAATAGCCATACCCACATTTGCCATTTGGCTAG AAGAACAATTTGGCAATGA
WI-11627	23	T C	CCCTTCCTCC ATTGCTCTC	CATTTGCAACC CACTCAAG	ACCCCTTTCCTCCATTGTCCCTC[G/C]CTTGAGATGGGTGCAATGGGAAGTAAAGCAAAAAGGG AGATGAGAAATAGTATGCTTTTGTCTGGCTTACTTCCATTCGCATGTCAGTCCATCCATG
WI-11636	61	A G	GGACTTAAAA AGATCTGCTTA	AGAACTTTGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAAATACTATTGTAAGGTGGACTTAAAAAGATCTGCTTATCCTT[A/G]TA TATCCACATAACTCTAGTGTACATAAAATATTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTTGTA
WI-11537	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCATTTCTTATGGTGGCAATAAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAG TATACAATATTAGAGAATATTATGTTGCAATTGCTCATCTTACTCTGACCATC[G]ATAATCATCTT TTTGCTGGGTCCAGGACC
WI-11654	37	G C	GCCAAAAGAC TATTCAGCAA	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAAGACTATTACAGCAACTG[G/C]AAACTGTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCGTGGTGTTCATACCTACTCAGAGTTTCACACTCATATTTTCATATTTT ATTTTGGGTGTTGGGT
WI-11656	28	G A	ATTGATTTTAG AAGGAACTGC	CAAGGCTTTGT CCTCAAGTAA	ACCTGATTGATTTTAGAAGGAACCTGCA[G/A]CTTTACTTTGAGGACAAAGCCTTGCCCTGCAGTTGTTT AAATGTCTGAAACAATCAGATTCCCAGCCTGGAT
WI-11680	55	T C	TTATCACAGC AGGGGACAG	---	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCTTTT[G/C]TTGCATAAA GGCTGGGAAGGTGGTTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAAACCTT	GTCCAAGAACAAAGATACTTTGACATCTTTATCAGACAGCAGGGGACAG[G/C]AAGGTTGGCTTCTCTA ATGCCCAACCATCTTGTTTTCAGAACTTTCCACTTCGCC
WI-11702	69	C T	GAATAATACT GAAATAACCA	AGAACAACCTT AAGCAAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACTTTCAATAATTAAAAATCGAAATAACTGAAATAACACACAGC AG[C/TT]TTCAGTATAATTGCTTAAGTTGTTCTAGAAACACTGCTAATTTTGTTCCTGCAGA
WI-11706	60	C T	TGGCTGGAATT TTCTCTTCTT	ATCACCAAAG AACAAATTCCA	TGCTGATTTCGCTTCTACCATCTGGCTGGAAATTTCTCTTCTTGTAACAATTTATTTGGCTG GAAATTTGTTCTTTGGTGAATTTGCCCTTTGCTGCT
WI-11709	105	T A	AGAAGCTTGC TTTACGTTGC	TCATTTCTCT AATTTTACGGG A	AATATCATCACTCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCCTTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAGCTTGCTTCAGTTTGC[T/A]GTCCCGTAAATTAGAAGAAATGAAT GGCCAGATGGATGGAAAA
WI-11710	103	C A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCCAGCTTTCCAGCAACACAGCCACACTCTAGACACGCCCTTCAC TCCAGTCCATCTGGCACCTAGCCTCAGTCTTCAC[G/A]CTCCTCCCTCCTCCACACACTCCTTC

WI-11715b	123	C T	AGCTT	AGGCTGGCTGC	TCCCATCCTG TGGCT	AGAATGGAGCTGTTGGGGAGGACATGCACACAATGTAAACACAGACAAAATGCATTACAACCTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGAGAAAGAGGCTGGCTGCAGCTTC/TAAGCCAC AGGATGGGACTGGGGAAGA
WI-11715a	49	A C AAA	AAA	GCACACAATG TAAACAGAC	CATTACACCAC AGTTGTAATGC A	AGAAATGGAGCTGTTGGGAGGAGGACATGCACACAATGTAAACACAGACAAA/VCJTGCATTACAACCTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCAGCCAC AGGATGGGACTGGGGAAGA
WI-11727	43	G C TCAACA	AAAACAACCTA	AACAATCCTT	CCTGTGGTTTG TGTTGCAG	CTGGATTTCTATACCTAACAAATCCTTAAACAACTATCAACA/G/CJCTGCAACACAAAACCCACAGGC AAATGAAAAACAGATGCCCCAGACAGCACCCACACATGGCACACAC
WI-11728	16	C G ---	---	---	---	TTTTATTATCAAACT/C/GJCAATTCATTTACAAAATGTAAATTATCATCAGCTCCCATCCAGCTTT CTCCCATCTCTATCTCTTTCCACCCCTACACTTTCTCTCCCTACAAACCCGGGTTCCAAA
WI-11758	61	A G TCGCTG	ATCTGTGGTTT	ATCTGTGGTTT	TGATTGGCCT GTGGTCTA	TTTTCTCTTTTATTAAAGTCGCTATACCTAACTAGAAAGGAGAACTGTGGTTTTCGCCCTG/AGJTAG ACCACAGGGCCATCAACCACAGCTCTTGTAGAGAACATGGAGAGTGCCAAAGATCACCATCA
WI-11295	37	A G AATATAA	GCCTCACAAA GTAFTTTCTAA	AAAAGTGCTCA TCTGTGAACCTC T	AAAAGTGCTCA TCTGTGAACCTC T	CCGGCCTCACAAAAGTATTTTCTAAAATATAATTTGCT/AGJTAGAGTTTACAGATGAGCACTTTTCA CATTAGGTGATATGCAACAAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93	T C ---	---	---	---	AGCATGATATTCTGCCCTGGAGTTTCTGTGAGCTCAGCAACAGCAGAGTCAGAGATTAAAGAATT ATTATTGCCCTCTTTTTCCTCCCT/C/GJGTGATTGTAAATTAGGAGTCAAGGCCAAAGTTA/C
WI-11282	42	C G GCAAGGAA	GGCTCAGAGA	AAAACCTCAGA CTGTAAATTTT GTGTG	AAAACCTCAGA CTGTAAATTTT GTGTG	CATGACAACCTCTTTTATTAAATGGGCTCAGAGAGCAAGGAA/C/GJACACAAAATTTACAGTCTGA GTTTGGCGCAGAGACCCCTCTCCACCTTTTCATGCCTGTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28	A G AAACCTCTG	CCCAACTTACC	CGGTAGGCGAG GCTAAGC	CGGTAGGCGAG GCTAAGC	TAATTCACCCAACTTACCAACCTCTGT/AGJGCTTAGCCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTTACAATGGGCAAAATCATCTAACACAAAAGC
WI-11879	61	C A AGTATACA	TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACTTT ATAAAA	GATAGTTGAAC CTCTTCACTTT ATAAAA	TTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG/C/AJGT GATTTCTCTCTTTCTTTTATAAAGTGAAAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91	C T AAGTTTAA	GTTTTAATGT GGTATTAGAA	CAATTTTCAGA TTGCTATAGC AAAC	CAATTTTCAGA TTGCTATAGC AAAC	TTTACTAATTTTCCATTTCCCTCTTTTATAGTTTTTAATGTGGTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATATCTATTCTA/C/TTTGACAGCACAGTCTTCAAAGTTTGTCTATAGACAATCTGA AAATTGGGTTCTGAACT
WI-11906	52	A G ATCTGAA	TGTTATAACAT CAAGAAAGA	TGTTATAACAT CAAGAAAGA	TGTTATAACAT CAAGAAAGA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAGAAAGAATCTGAAT/AGJTGAGGGAACTG CAGAAATTAACCTTCAGTCTAATCTCAGAATGCCAGAGTAAGATGAACCTTTACAG

WI-11909	78 A G	TTTGTTGGG TGGTCAAG	CCTCCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAAGACAAATGGATTGTGGAGCATACTGAAGACTATTCTCTAAATGGCTATTGTGTGTTG GGTGTCAAG/A/GCTATTAGAAATCTCAGAGGAGGACAAATGATAGTCACTGCAGCCAGCTCG GACTGGCTTGCAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCAATTTAGCATCAATTTGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA/T/G/GTT TTATTAGTATATAAAATGGCTTTACAGGAAGCATTTATGG
WI-11946	31 C A	---	---	CCCTAGTGAATACAACCTTTGTCTCTGGAGAC/C/ACAGCTAGTCTAAGAAAACTTCTTAGGCTGAG CTCTCTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAAGAGGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTTT GATT	CAGCTGTGGTG AATGTTGAT	ACAAAAATCACAAAGTACAACACTGCTTATTTCTTGCTTGAAGATCAGATCTCTGGTTTATTTAA/T/ GATCAACATTCACCACAGCTGAAGGAAATTAACGTGAACCT
WI-11027	90 T A A	TGCCCTACTAC GCTTTTAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAACCTGCAGAAAGGGCAGGACAAAACAAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAAT/AJAATAAAATAGCTGTAAACACATTTCTCATTTCTCTTACGA ATACCTTCTTTTGATATTGCAATTTCTATGGCATACACAGAGGCACCTCTCTCAATGCCCTG
WI-11049	95 C T	---	---	TTCTGCTGAAGATCACAAAACAAATTTCAACCTCTGTGGTTCAAAATTAATTAAGGATCTTGTACCTTT GTGTTATTTCTGTTTCAACTAAGGA/C/JAGACTTCAGAAGGCATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTCAITTTGAGGAAGGAACATTTCAAAAGCCCAA
WI-15488	69 C T	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGGAAAAGTTCTCACTCTGCACATATAAAAAGGACAGCCAGATATCA AC/C/TGTTACAGAAATGAATAAGATGGAAAATTTTAAACAAATTG
WI-13654	49 A G	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGT/A/GJGTATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAAGGTAACTTTTCCCAATTTACAGACAAAACCCAGT
WI-11070b	135 C T	---	---	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAAAATGTGACTGAGCAGAAAATCAGCCAGCTATCTTGGTGCAGAGAGGTACTCCAAAGTA C/C/TJGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAAAGGAA
WI-11070a	110 G T	CAGAAAATCA GCCAGTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAAAATGTGACTGAGCAGAAAATCAGCCAGCTATCTTGGTGCAGAGAGGTACTCCAA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGATCCAAACAGAAAGGAA
WI-12020	121 T C	---	---	AATCTTTTATATTTCCAGCTGTGAGACAGTATTTTGAGGGCTGATGTTACCTCTAGCGGCGAAACC AGAGCCAGCTATTAAAGCAGCCAGAAAGCTACAGTAATTAATACATGACCATTT/CJCTCTTTTAGC ACGTTCTTTGTTCTCCTG

WI-11076b	142	G A ---				CATGGTTCTGCCAGCTTACAGGAAGCATGGTGTGGCATCGGCTTATCTTCTTGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGGAGCAGGCATGTACATACCCAGAGCAGGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT
WI-11076a	106	T C AGGCA	AAGGGGAGC	TCCTGCTCTGG GTAATGAC	---	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGTGGCATCGGCTTATCTTCTTGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGGAGCAGGCATGTCTACATACCCAGAGCAGGAGAG GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT
WI-14263	49	T C GGCAATATCA	CGCAGAAAA	AATTAGTATGG GACA	---	ACCTTTAAAGTTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAA[G/C]GTGTCCCATACTAATT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA AATTATTGCTGAAATTAGGAAGGAGCA[G/C]TGAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAGCAAGTACCATTTTCCAAAGTATAAAACCTCGTA
WI-14267	28	T C ---	CTTTTCATTT TGCTTTTAA	TGATGATGCA TATACTAAAA ATCAAAG	---	GATTTGTTTTATTTCATTCGCTTTTCATTTTGCTTTTAAATAGAACAG[G/A]CTTTGATTTTAGTA TATGACATCATCATCATGAATTTTCTCTTACTTTGTTATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-15288	108	C G TTCCCTCTCTC	CATGAGAGGA	AAAAGCTTCTT TCCCTTGA	---	ACCTCTTCTGATGACACTGTACCTGTAAAGGGGTCTAGAGAGAAAGAGTAGTAGCTCTACTTTGTC TACAATTCAGGATGCAGGGCATGAGAGGATTCCCTCTCTC[G/C]TCCAAAGGGAAGAGCTTTTGGC AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAACAGACCCAGATCAGAGGAAGAGATG GCTTCTTGTTAATTCTGGAGCA[G/C]ATTCAAGCAGCAATATTTACTGAACACTTGCTAIGTCTG
WI-13951b	88	G C ---	GGAGTGAACA AAGTAATGAA	---	---	G AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAAA[C/TA]GACCCAGATCAGAGGAAGAG ATGGCTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAATATTTACTGAACACTTGCTATGTGCTG
WI-13951a	39	C T CAAA	AAAAAGGCTC TTGCCCAT	TTCTCTGATC TGGGTCT	---	G GAGACCAAAAAGGCTCTGCCCAT[G/TA]ATTCCCGTCTCTCCCTCCTGACTGACCCCAAGTGTCTT ACAATGAACATCCCTCAGCCCCATGGCATGGTGCATCCCCCTCTCTTGGGATCTGTGAATATAACCA ACTGTCTTGTCATGGC
WI-13264	25	G A TTGCCAT	AGCAAAAAGGA AGTTAAATAC	GGAGGGAGAG ACGGGAATA	---	TTATTTGTCATTAGCAAAAAGGAAGTTAAATACTGATAGA[C/TA]GATGCAAAATTTGCTCTTCATGCA TTTGTGGAGCAAAAGTACTAATTGTTCACCTGTCATTTCCCTCACAAGGAGTTGAGCCCCCTAGATGAC
WI-13960	39	A C TGATAGA	ATCATTATAACC AAGAAGCCTT	CATGAAAAGGA CAAATTTGCAT C	---	AACTCTTTATGTTTAGCTAGCCCCAGTGACTTTATGCATCTTATAACCAAGAAGCCTTCAG[C/TA]G AGCAAGTCTGAGCCAGAGGTTTATACACATTTGTCTCAGGGTCCACCAGGAACCCAGGCTTGGCT
WI-15943	62	C T CAG	ATCATTATAACC AAGAAGCCTT	CTCTGGCTCAG ACTTGTCTCT	---	AACTCTTTATGTTTAGCTAGCCCCAGTGACTTTATGCATCTTATAACCAAGAAGCCTTCAG[C/TA]G AGCAAGTCTGAGCCAGAGGTTTATACACATTTGTCTCAGGGTCCACCAGGAACCCAGGCTTGGCT

WI-13983	52	G A	TCCTCCCACT CCTTAAACCT	CAATACTCTCT TAGCCCACTGG	TTGTGTATCTGATTTCCGAAACATAGAAATCTCTCTCCCACTCTCTAAACCTTG/AJCCACTGGGCTAA GAGAGTATTGTACAGAATATGCACTCACTGACTTAACAGAAATTAGAACATCCAGGCACCTCACTGAGA
WI-13850	51	A G TT	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTGTAA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTTTAACACAGCCATG/AJTTACAAACATTGT CAGGGAACATTTACAAGAAATAAATAGATGGACTTGACGGGTGTAAGAAATTACACTTCA
WI-15295	27	G C A	TGTCAGTTTGA ATGTATTCTCTG	TGAATAGTTGG CAAAGGAAA	AGATGTCAGTTTGAATGATATCCCTGATG/CJTTTCCCTTGCCAACTATTCAATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATACAAGAAAAAGGCCCGAAAAATATGAGTGAGACTCA
WI-14284	55	C T ---	---	---	AATTCAAACAAATCCAGAACAGGTTCTCACACITTTGAGCCCTTAGTGCAAAAACA/CJTTATGCCAT GCGGGAATAAATGCTTATCCAGTGAGGCTCCCTGATGCATTGA
WI-14288	85	G C	CCGCTGCTATT CCAGAT	GGTCTCTTCC ACCAAATCTT	ATGACCAGACCAGAAAGCCCTGTCTATATGAAGACAAACAGGTGCCATACCTTGGGTGGAGGGGATA CCGCTGCTATTCCAGATG/CJAAAGATTTGGTGGAGGAGACCATGACAGATGACAAACGG
WI-13522	33	C T	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTTGATGTAGTTACCCCACTAATACAAC/CJTGAGAACCACTGACTTCAATATTATGAGAG AAATTTACTCCAGGGAATTTTGCAGAGAAGATAATA
WI-13529	42	T C	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCCATCCACAACATTTATTTGAACAGTTTACCAT/CJAAAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCGAGGGGTTATAGTCTAACAGGGGAACAACCTCTCTC A
WI-13859	84	G A ---	---	---	TTATTTGTCAGAAATTTCCAGAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAAAGGAAACTATG/AJACAAACAAGTATATATTGAGGAAAGGACTCCTAGAACTTGAGCA ACA
WI-13536	29	T C ---	---	---	TGAAAGGATACAGAAAAAATCAGCGAAGT/CJGAAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAAGCTTCCAGTTGTCTCTCCAGTGCCATTTACATGGAGTACACTTAATTTCTCAGCA
WI-13373	52	G A ---	---	---	TTTATTGTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCACG/AJAACTGTGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCCTTTGACGCGGGCCCTTGAATCTGACATTTCAAGTCAC CGTAATAGAAACCAGAGCT
WI-13477b	61	A G ---	---	---	TTGGTTTTTAATACCTCTTGTGGATAAAAGGACATTTTTCATTAGCTTGCTTCAAA/AJGJGAC AGAGAAATAAGATAAAATTACCTTAAAGAAATTAAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCTCAGTT
WI-13477a	32	A G AAG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTTGTGGATAAAAGG/AJGJGATTTTTCATTAGCTTGCTTCAAAAGAC AGAGAAATAAGATAAAATTACCTTAAAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACITTTATTAGCATGCAATGCAATTTATTCTGGCAATAAATAATATATGTCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAG[A/T]AAAAATGTTTCTGAATGTGCACACTAGATAATATATGCAAGATCCTTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTACCATTAAGAAATCAACA TGTGCACAAAAAGAGTAAAAAT[T/G]ACCACAAAAATTAAGATTTTTGGGACAAATTCACATGTTG AAAAAT
WI-13582	43 C A	TGCAATCTAG AGACTGGGA	TCTGCGCAGTT AGATTCCA	AAGGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[C/A]TGGAACTAACTGCGCAGAG AAATCAAGACOGATGGTGAAATCTGGGCGAGCTTCAAAATTTCTGCCTCCTAAAAACATTTTCAG CCAAATTTTCATTATTGCC
WI-13857	28 A G	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTTAGGTATCTGGCACAAATTAACCAATGT CTGCCATTTTGTGTAGCTTTTCATACAGTACAGATTTTCATTGATGTCGCTCCACATCTG
WI-15809	77 T G	TGTTTCTGT TGTAATGCC	TAAGTAGCTA ATTCAATGTTT GTAAA	GTTTAAAGTTCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAATGCC[T/G]TTTACAAACATTGAATAGTACCTTAAGTATTGAAGAGCTTCCATT
WI-15809b	123 A T	---	---	TAAATCAGTCTGTGTCAAGAAAGAACAGGACTTGAATCAAGCTTCCAGCCCTCACCACCTATCAGCA TAGCAATTTTAAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAAAGAA[A/T]GGAATCA ACTCCACAGATCAACATGT
WI-15801a	81 T G A A	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCITTTATTCCAAAGATGGGAAGCGCATTTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACTCTA GCTGCAGTAATAC[T/G]GCATCCCATCCACTCTCTCTCTCTTTTGTACTGAAACTCTTCAAGAACT GCTGAATGTCCTCTCTC
WI-15801a	24 G A	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	TCITTTATTCCAAAGATGGGAAGC[G/A]CATTTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACT CTAGCTGCAGTAATAGTGCATCCCATCCACTCTCTCTCTCTTTTGTACTGAAACTCTTCAAGAACT GCTGAATGTCCTCTCTC
WI-13763	59 T C	GGCTGGACACT GCAGTGAT	CCACACCTGC OCT	GCTCGTAATGAGACAGAACGCTACATCTGTTCAACACTGGCTGGACACTGCAGTGATT[C]AGGG GCAGGTGTGGGCGAGGTGGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA TTTTTTTTTGGTGAGTGTGTTGCTTCAATAAAGAGCAGAAAGAAACCC[T/A]AGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCAACATTTGATATTTTGTCTTTTCCCGAGGGCAAAAAGA GAGTCTCCACAGAAACCTC
WI-13578	48 T A A C C	TCATAAAGA GCAGAAAGAA	CAGTGTGAAG AACATCTTTT GTC	TCCAAGGAAAAGAAAGAAACCAATCAGTGAGAAAACCTCAAGAAATGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTAGGGTCCCTCACTCTCTT GAGGTCCCT
WI-13789	62 G A	TTGGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTT	GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTAGGGTCCCTCACTCTCTT GAGGTCCCT
WI-13594	66 G A A G C	TTTTTAACACA GATCACAAAA	CCTTTGCGCA GTACTTTT	AATAACAAGTTTAAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACACAGATCACAAAAAGC[ G/A]TGACAAAAAAGTACTGGCGCAAGGACAAAAATAATGCTAAGAAATTAGCCAAACAGCTGC

WI-15625	40	C T ---	---	GTCTCCCCACCTACTCCCGGAGAAAAAGGATATTCAA[C/T]GTCCCATCTAATTTTTGAATAA CCTAACTCTCCCTTTGTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84	C G A	CCACACTGAA GACTCACACAG CCCT	GTCTCACTTCTTGCTAGGCTGTAAATTTTCAGTTTAAACAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACAGAA[C/G]AGGGTGGGTGGGAATACTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCCT
WI-13600	26	G T	TTAATGAGCC AAGCATCCAT	CTCACITTTAATGAGCCAAAGCATCCAT[G/T]CCATCATCTAGTAACAATTTTCAATATGCACATTATAT TATACTGGAACAACAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATCCCTTCCTACCC
WI-13602	89	G T	TCCATTCTGGA GACAACACA	GATAGGAAAAGAAGAAATGAAGTCAATAGTCTTTAGCAAGCCAACTAGTCAAGGAATAGACAGCCC CTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAATTTAAATATTGTCTATGAGGTATGCACCT GCCC
WI-13650	76	A T	AAAGATTAC AATATTTCACT TTTAAAC	GCATTAAACATTTAAAAATCTGAGGGATATTTGATGAGAACTATGATGAAAGATTCAACAATTTTCAC TTTTAAAC[A/T]TAAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAGTTACCCG
WI-14319	83	C T A	CAATCAAGG CACAAAGCTA	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGACAGTACAGAATT
WI-13528	80	A G AAAA	CAATACATTT GCATTTTCTCTA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAACTGTAACTAATCAATACATTTGCATTTTCTTAAAA AAAGAAGACATTT[A/G]TTTCAGAGAAAACTGGGTATCATGCGAGGAAAGCAGAAAAAATTT
WI-13909c	93	A T ---	---	ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTCCAGTGAAGTTTCATCTTCTCAGACT CTCTTCAAACTCGAATATCTTTTTC[A/T]GAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80	G A C	TTCTCAGACT CTCTTCAAACT	ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTCCAGTGAAGTTTCATCTTCTCAGACT CTCTTCAAACTC[G/A]AATATCTTTTTCAGAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86	C A ---	---	TTTTTATTGAATCCAAATGTAGCAAAATCATTTAAACAAATTTATAAAGGGACAGAAAAATTAAG AATCAACATCATCTGGAC[C/A]ATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-14323a	78	T C ACATCA	ACAGAAAAAT TAAGAATCAA	TTTTTATTGAATCCAAATGTAGCAAAATCATTTAAACAAATTTATAAAGGGACAGAAAAATTAAG AATCAACATCAT[C/T]CTGGACCATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-15389b	104	G A AAA	AGATAATGAA ACATCTGCGA	AAAATTGACAAATCAACTAGCTTGTCTTTTGTCTGTTTGGAGACTACCATTTATTCAAATTTATTTATGT AATACACTCATCCAGATAATGAAACATCTCGGAAA[G/A]AAGTGGGAATCACCTCACTGTGTC

WI-15389a	33	A	AATCAACTAG CTTGCTTTTG	TTTGAATAATG GTAGTCTCCA AA	AAAATTGACAAATCAACTAGCTTGCTTTTGTG[C/G/A]TTTGGAAAGACTACCATTTATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAAACATCTGCGAAAGAAAGTGGGAATCACCTCATCTGTGTC TGTAATCTGCTTACAGTCCCTTTGCAAGACAGACATATGTTTTTGCATAAAGATATAAATTGCTTCAT TTTAAACTAATTTAGTGTTT[C/G]TTTAAATTATATGAACCTTTTGGTGAATTATGAACCTGTACCAAAC C
WI-15747	88	T	AGTGTTT	CATAATTACCC AAAAGTTTCAATAATTT	AAGAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTCGGATGAGTTCTCTCGTTAAGTGCTGGATATACTTGGCTTGAC[C/T]GGACACCTTTTACG GAGGATTCGGACAAC
WI-13752b	117	C	---	---	AAGAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTCGGATGAGTTCTCTCGTTAAGTGCTGGATATACTTGGCTTGAC[C/T]GGCTTGACCCGGACACCTTTTACG GAGGATTCGGACAAC
WI-13752a	106	T	AGTGCTGGA	CCCTCTCGTTA AGGTGTCC	AAGAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTCGGATGAGTTCTCTCGTTAAGTGCTGGATATACTTGGCTTGACCCGGACACCTTTTACG GAGGATTCGGACAAC
WI-14339	102	T	TTAG	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCCACCAATCAACAGTACATGATTACTT[G/C]GGTTCCAGAAATCTGGATAC TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAACACACGTAAATGGAACCTTCATGCAGCTTTAGAT TTCCCTTGCCCGAGTAGGAGCTTGTGTATGGTCTGAACAAAACCTGAAC[C/T]GCTGTGCTTATCTTTC CTGATTCT
WI-13744	115	C	AAACTGAA	GC	CCTTGACTATATTGTTTTTCCAAAATAGGACTATGTAGAGAGAGAGCCCGGTACATACCTTAT [C/T]AACCATTTCAATCCACCATTTGTAAAATCTCATCTTCTGGGCTGGATACCTCAAAAACAGAT
WI-14061	68	C	---	---	TTACAGTTGGATTAACTACACACTGAATATACCTGAATTTAACTATTCAACCCCTTTCATCCATTGAG C[A/C]AATTTAAACTCTTGCCCAAGTATCATGAACCTACGAAGAGGAGATAAGAGATCTGATC
WI-15719	69	A	CATTGAGC	ATT	TAATCCATCAATCTAAAATCACACATACATAGATCAAAACAGAAAGTACCACAGTATGCTTTATTTGCA GGTATTAAATGGTTCTCTAAATCGATACATCCAAAACCTT[C/G]AGTTAGCAGCAAGCATCAGTTCTTC
WI-13810	106	T	CAACT	GAACTGATGCT TGCTGCTAACT	GGATTTATTACATTAACTTGACACAG[G/T]TAGCAAAAAAATCAAAAACATAAAACTAAGCCACA TATCAAGAACAATATACAATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA TCAAAACGTCACACTATAAAAGTGCTTTAAAATGCAGCAGCAGGAGATGTGAAGACACAAAATGAAC AAGTG[C/G/A]TAGTGACACATAGCTGTGCACAACACAGTG
WI-15736a	27	G	CACA	TTT	TCAAAACGTCACACTATAAAAGTGCTTTAAAATGCAGCAGCAGGAGATGTGAAGACACAAAATGAAC AAGTG[C/G/A]TAGTGACACATAGCTGTGCACAACACAGTG
WI-13785d	72	G	---	---	TCAAAACGTCACACTATAAAAGTGCTTTAAAATGCAGCAGCAGGAGATGTGAAGAC[C/A/C]CAAATG AACAAAGTGGTAGTGACACATAGCTGTGCACAACACAGTG
WI-13785c	56	A	---	---	



WI-13785b	40 C	G ---	---	---	TCAAAAGTGCACACTATAAAAGTGCCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAAATG AACAAAGTGCCTAGTGACACATAGCTGTGCACAAACACAGTG
WI-13785a	27 T	CTGCTT	---	T	TCAAAAGTGCACACTATAAAAGTGCCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACAAAATG AACAAAGTGCCTAGTGACACATAGCTGTGCACAAACACAGTG
WI-13793	88 C	GATAGG	---	GGCAGGAGGA TTTGTTACT	AGAAACCAAGTATATCATAGGCCAAATAAAAATAGTTTTACCCCAATTGATACAACATAAGGGATTT TACATTGAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCCAATAATCTATGACTTG
WI-13794	52 A	GTTCTTCTC	---	AGAATGGGCTC TTAACCTTGTA	TAGTCTCCTACAAATTCCTTCAATCCATTTTCTCCTCACCCCTTTCTTTCTC[C/J]TACAAGGTTAAGA GCCCATTTCTTCAACAAACAAAACACATAGAGCAAT
WI-15729	35 A	GCTGAGACTGC	---	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[J/G]GGGACTTTAGAAAGAAAGCTGAGACTGAA AAGTCTGCTTGACTTCCAAGGAAGGTAAAGTCCCTGTTTGCAGCCCCGGGCTGCTCATTTGTTA
WI-13424	66 G	A C	---	TTTTCTCCCC AGGGTCTA	GTCCCTTGCACAAAGTCTCCCAACTGGTTGGAGTTTCCCTTCTGAGGTTTTCACCCCTATTCTTC[C/J]A JTAGACCCCTGGGGAGAAAACACATGTGTAAAGTGCTCAGGACATGAGGCAGGCCGTTTCAACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29 T	CAAT	---	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTCAGAGGCAATTT[C/G]AGATCCCAGATTCAGCTTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAATTTCTTGCTGCTTTTAAATCCTGAACATTTCTGAAGCACAGAA
WI-13446	22 G	CTACTCATCA	---	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTCACTCATCA[C/G]CCTTCTGATTTTGATTCCTTTCTGCTCTGTAATTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTAGAAATTTCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAAT
WI-13725	56 A	CTGGTGCC	---	CCTGCTGCTC GGGC	TCACACAAAGGCATTTGGAAATGTCACTTACACATGGTGAGCACATATGGGTGCC[C/J]GCCCGAG ACAGCAGGATAAGTTTCAACAAACTTGACCAGGCAGGTAGAACGAAGGCATGGTTCAAGGATG
WI-15702d	107 T	C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAAACAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAA[CTAAT]/[C/J]GGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101 T	C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAAACAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAACT[C/J]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90 C	T ---	---	---	CAAATGTTTTATGAAGAGACTCCGAAACAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAACT[C/J]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA

WI-15702a	48 G C A A A G	A A C A A A A T A A A G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A A T G T T T T A T G A A G A G A C T C C G A A C A A A A T A A A G G C T T T C A A A A A G [G/C] G G G T A A A G G G G T G A G G A A A G C A T G T G A G A A A C T G T A A C C C T G T A A C A A T A C T A A T G G G T C T T T G A A C A A A T A G T T T T G A
WI-13831b	113 T C ---	---	---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A G C G A A G G T G A C T T G G A A A A G G A A G G A T T C A C A T A C T T C C A C T G T A T C C T C G G G T A A G T T T C C T C T C T C T G T A G A T T C G T C T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13831a	56 G C ---	---	---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T C C A C T G T A T C C T C G G G T A A G T T T C C T C T C T C T G T A G A T G T C C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13806	62 G A ---	---	---	T G A T T G A G C T T A G A A G G A A G T C A T G T T G A A T C A G A G A G G C C A A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A A G G A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-14372	86 A G ---	---	---	C A C A T T T T C A G C A A A C A A A T C G A G G T G C A A A C A G G G T T A T T T C A C A T T A A T A T A T A A C T G G A T T T T T T G C A A A T A A A T A G G G A [A/G] T T C T C T T T A A A T A A C C A T C T C C T C A C T T C A T G G C C A G T
WI-14373	95 A G ---	---	---	A G G C T G T T T T T G A G G C C T G A G G C C C C A C A C A T G A C A C G T A A G A C T G T A A C C A T G G T C A T G T A G T T A T G A G C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C A C C T C C C A A C G C C T T T A C T T T C A C A G C C T C T G C A
WI-14078	61 C T G C A A G	A A A G A A G T A A A T T A G G A A G A	T G T G T G C A T G T C T C T T A C T G C	A G A A C C G A G A A C T C A A A G A A C C A C A C A T G G T G T A T C A A A A G A T A A A T T A G G A A G A C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A C A A G G G C A T G G A G G A A G G A C T T T A G A T G G T C A C G
WI-14083	47 C T A C A C T	A G A C T T G A G A G C T T A A A A C A	G C C T A C T G G A C C T C T A A A C T A C T G A	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A A C A A C A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T G C T T A A G G T C T T A C A A G G C C A A
WI-14085	31 A G A G A A A A	C A T T T A T T T C A T G T G T A A G A	C A G T C A T G T T C A C G T G C T A G T T	T G C A T T T A T T T C A T G T G T A A G A A A A A A C [A/G] T A A C T A G C A C G T G A A C A C A T G A C T G C A T C G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A A C A A A A T A G C A T G T T G A T T T A A G T G A A A T A A C A G A A C A G G A G G C C T T T
WI-12169	121 G C T T G C T T	A A T A A A A C T T C C T A T T T C T T	G G G T T C T G A G G T G A A A G A A A A A	G T C A A A G G T T G G C A A A T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T T C A T T T C T A A A T T T T C A C C T T T A T T G C T A A G T T A T A A A T A A A A C T C C T A T T T C T T T G C T T [G/C] T T T T T C T T T C A C C T C A G A A C C C C C T T A
WI-15705	50 A G A T C	G G A G G G A G A T T T T A G A C T G A	A G C T G T A G T C G T C A A A T A C T C T A G A A	T T G T T T T A T T T G G G G A A T G A A G G A G G A G G A G A T T T T A G A C T G A A T C [A/G] T T C T A G A G A T T T T G A C G A C T A C A G C T C T C T C T T T G T A C T A C G G A G A C C C T G C T T A T A G C C C C A A C A G A A A T C C T C A T C T G C G G T T G C C A G A C A G

WI-14379	102 C T	TCTATTAACA GGGTATGTCA CACC	ATCATCTGTT TGAGGTGACA ---	TTTATGCTGTTGTTTCTACTGGTGGTCTGGCTCACTAATATCAATCCTAGTAGTATTTCTTT TACTTGTGCTATTAAACAGGGTTATGTCACACC[C/T]GTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAA[C/A]CCACCAATTAAACAAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCCCGAGGCTGGCGCAGGACTGCCACTCACCTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22 C A ---	CGCAGAGCTG CTGTATTTAAA	GCAGAGATCCA GACGCTGT ---	ACCGCAGAGCTGCTGTATTTAAA[A/G]JACAAGCGTCTGGATCTCTGCAGGGCTGGGACCAGCTGC AGTGGGGCTCCGGCACTGCTCTCTCCAGGACTCTTCCACACCC
WI-15937	24 A G A	AAACTGAAAC GTATTTCTCTC	GGCCTTTAAGT TTCTACGGTG	TGAAACTGAAACGTATTTCTCTCA[A/C]JACACCGTAGAAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGCGGAAAAAGGAAGTTTCAGGTGATACAAGATGTCCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24 A C A			ATGTTTATGATCAATTCAAACATACAGTACAGGGAAGGTGAATGAGTAAGAAAAAATCAT ATTTAAGTCCCCGTTAACACTAAGCC[A/G]TATTATTCAAATGTGTTTCAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14124	92 A G ---		---	GACAAAGAGGCGAGTTTCTGTAGTTCACAGAGGGCCAGAGCAGTTATCAGAACGGTGGTTGACCT GCATAGATTTTGTGACGACTA[C/T]GTGGCCATGCCATTCTGTAAAGTGAAATTAATGAACA
WI-14125	88 C T CATAGATTTT	GGTTGACCTG CATAGATTTT	GGAATGGCATG GCCAC	GTTTATTTCTCACAGTTCTGGAGGTTAGAAGCTGAGATGAGGATATCACAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTCTCACCATGCTTTCACAT[G/A]GCCCAAAGAGAC AGAACAGCTCTCTGGT
WI-14136	120 G A ATGTCTTCACA	GCTTCTCACC ATGTCTTCACA	CTTGTTCTGTC TCTTTGGGC	TTGTTGTTGGCACCAGAAAAGCT[C/T]ATGTTCTATGTATTGTCACCTGTACATACTGTAAACAAGACT GCATTAAATATGTTTCTTATGATTGTTTCAATG
WI-14138	23 C T GAAAAGCT	TGTTGGCACCA GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	GGCAGGTTTATTCATAATTTCAAACITGGAAGCAACCAAGATGCTCTCAGTAGTAGTATTTCA GACAAATC[G/A]AATATTACTTAGCACTAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-13551	74 G A GACAAATC	TCCTTCAGTAG TAGTATATTCA	GCTCATTTCTT TTAGTGCTAAG TAATATT	TTTTTTAAGAGTGCTCTCACATCATTTATATTGATTGCACAAAACCTTTTTTAACCTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTOCC
WI-15953b	59 C T ---		---	TTTTTTAAGAGTGCTCTCACATCAT[T/G]TATATTGATTGCACAAAACCTTTTTTAACCTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTOCC
WI-15953a	26 T G A T A	TTTTAAGAGTG TCCTTCACATC	TCATCTGTTCT TGTTGTTTTTG A	TTTTTTAAGAGTGCTCTCACATCAT[T/G]TATATTGATTGCACAAAACCTTTTTTAACCTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTOCC

WI-14631	82 G A ---	---	---	TGAATCAATGGACAGTTTGGCTCTGTTTAGTGAAACCCCTCACAAGCACTCTGCATAGTCCGCTTT CTGTCTCTTTAAAC[G/A]TGCCCTGGTCCCTCTGCCAAACCTTTTAGGATTGGGCTCCTCAGGGCGCTT GTCCTGA
WI-6053	24 A G ---	---	---	ATCACCCCGTGTCTAAGAACAAAC[A/G]CTTCATGTCCAACTCATATCCCGGGAGCTTTGTCAACTG CAGTACACTTCTCGCATGAACCTGGCTTCTGGAGGAAGCCTCTAGAGGCCAGGTAAGGGGGTGC AGCAGTGAGGGGTATATCTGGCTGGCCAGTTGGAACCCAGGAG
WI-15964	99 T A CTGGAGGTA	GACTTCTCCAC OCTCTTGC	---	CAGAAACCTCTTCTGTGTTAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCAGGAGGCTGCCTT GGGAGGTAGTAAGCTCTCTGCTCCCTGGAGGT[A/G]GCAAGAGGGTGGAGAGTCTTGGCAAG
WI-12075	103 G A GGCAC	AGCAGCTGGG TCTTCTTC	---	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAAGCAACAAAGCCAGGCAAAATACCCATCAG AGACAGTGACAAGAGCAGCTGGGGCACGGGGAGGC[G/A]GAAGGAAGAGAAAGAGGGGAGGAG OCT
WI-12179	96 G A TGGAGGTCA	TCGAAATGACCC TGTAATGC	---	TAATTTAAACACGCCCTTCCACATAGTGGTGAGGCATCTGCACATTTCTCTAGAAGGACATGA ATAGTGATGTGGAGGTACGGTGGAGGTCA[G/A]GCACTACAGGGTCACTCGAGGAGGAACAG
WI-14651	49 C G ATTGT	CAAGAATCAT TCATTTTCTGA CTTATTT	---	CACAAATAGTGAAATTTATCTGAGCAAGAATCATTTCAATTTAAATTTGTC[G/AAATAAGTCAGAA AAAGATCAATATCTCCCTGCTTCAAAATGACACTCCCAATTTTACAGGTAACTGTTA
WI-14666	105 T A ---	---	---	AATGTGGACTTCAACAAGGGTTTAAACCTAATCTAATAACAATCTTACAACACATTTCCAGAGCAT TATAACAAGAATTATTTACAGGCAGCTAATGTATTAAAT[A/A]AACCATGAAAGGAAACAACTTG
WI-13473	31 C T ---	---	---	ATCTAGATGCAGCAATGGGCTGAGACTGTC/TGTGCTGGTAGAGTGCAGTGTGTGTATGTTCTAC TCTATTACAAAATTAACAGAAATATGGCTTCGCTTGTGCAATGTTTATATACAGTC
WI-13967	103 A C AAATAAAA	AAAAGACTAC AGATACAAAG TG	TTGTGTTTCA TCTCCTAAAAG	AAATTAATAGCAGCTCTGTGTGTGATTTTAAAGAACAGATAAAATAIGTCATTCAGCAGTCATTT AAAAAATAAAGACTACAGATACAAGGAAATAAAA[A/C]ACCTTTAGGAGATGAAAACACAAA
WI-14408	60 T A G	GCAGACACAC TATTACAGGCT	TTAATTGTGA AAACTCATTTG TTACTTT	TTAATATTTAGCAAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTG[T/A]AA GTAACAAATGAGTTTACACAATTAATAATTAACACATACTTATGGGATTTGTTGAATGA
WI-13683	47 C G ---	---	---	TTTTGTGTTAAGAACAGCATTTTGAAAATAAAACCTATCTGCCCATG[C/G]TTTACAGCCTTTTAAAT TTGTAATATTTAATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63 C T CGTCT	CACCATGGCA CAC	CATTGAGATAA AGCACACTTAT	TTAGAAAACCTGATAAAAGCAACAACTTTTGGGAAAGCACCATGGCACGTCCTTTGTGCTA[C/T] GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
WI-14635	22 G A ---	---	---	ACATGGCAGATACAGAGCTG[C/G]ATCTTGAAGACCACTGACCAGGAAATGCCACTTTTACAA AATCATCCCCCTTTTCATGATTGGAACAGTTTCTGACCGTCTGGGAGCGTTGAAGGGGTGACACAGC ACATTTGCACATGCAAAA

WI-16002	59	T C	GATAACATAA AATGATCATG AGAAATTC	GCCATCTCCTC TTTGACTTTT	CCAACATTTTAAACCCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTTCA[T/C]GTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGGCT
WI-15361b	101	A G A	CCCACTTGAAC TCAAGTCATC AAA	AAACTAAAC CTTTGTGCTA AAA	GTGGAATTTTATTAAAGCCATCAAAATTTCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAACCTCAAGTCATCA[A/G]TTTAGGCACAAGGTTTGTAGTTTCTCGG GAAATCAAGTTTAAACCA
WI-14759	73	T C	GGGTTGACTT GTGGG	TCCCACTGCG OCC	TGAGTTACAACAATAAGCAACAAGTTAGAAAAATGGTTTTTATTCAAACCTCCTAGCGTTTGACTT GTGCGG[T/C]GTACTCAATGGGGGCGAGTGTGGACGGGAGGATTGCAACCAAGAGTTTCATACTG CAA
WI-12535	50	A T T A T	CTAGGAGGGTT GAGGTGTAGA	GCTCCACGAGA AGAGAGGAA	TCCTAACATTTATTCAGGTGGTACTAGGAGGGTTGAGGTGTAGATAT[A/T]CTTCTCTCTCTC GTGAGCCTTACTGAAGACAGGATGCCGTTCTTGTGTTTATCAGCTGAGAAGGGCAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112	G A	AAAGGCACAC GGGAA	CTCAGCCTGCG TTGACC	TTCCATTCAATTATGCTGGCTTTACCAATTTTATAGCTATTGGGAGGCAGGAAAGGAAATTTGGG CCAGAAACCATGAGATTTGGGTGAGAAAAAGGCACACGGGAA[G/A]GGGTCAAGGCAGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18	T C	---	---	ACACAATAAATCCAT[T/C]CGAGTGATTAAAACTATTGTTGTTTAGAACCAACAAAACTAC AAGAAACATTTTCAAAACCTTTTTTTTCAGGCTGA
WI-14808	52	T A	ACCACCCACA CTACCTGT	ATGTTAAGATT TT	CTTTGAACACTTTAAGCAACAGTTAAAAAGTACCCACACACTACCCTGTT[A/JAAAACTCTTAAC ATTGTGATGCCTCTGCATCAATTTTAGAAAAACAAGAAAAACAACAACCTGAAGGCCCATGTA
WI-14816	29	A T	---	---	AGTTAAAAAAATCGAGTCAGCATTTTATT[A/T]AAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAATGCAATTTATTTGTATCCCAAGCCCTGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAAGCTACGACTTC
WI-12542c	71	G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70	G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45	C T	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTTCTATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57	C T	GGATACAGCA GTAAAGAATA CAAAA	CCACCTCTAGA ATGATGCTCT ATAA	CACCTAAATCATCTAGAAACTGGGGATACAGCAGTAAAGAATACAAAAATCCTG[C/T]CTTATA GAGCATACATCTAGAGGIGGGAAAGAGGCAATAAATA

WI-14836	28 T C ---			TC TTG GAG GGA TAG AGG ACAG AGT GTT C/G TTT GATT TTT CG TTT CGG TTT CAG TTT GGT TGT CATT GG TTT TTT G TTT TTT GCT AAT TTT GCC CCA C C C T A T A A A A A G C A G T G C C A C C C A G A G G C A G
WI-14856	60 A T A A		TGGTGACACG GAAATACTT	ACATTCC T TATGATAGCAACAAC TAAATATGATGGATGGTGACACGGAAATAC TTTAATATATTA AGTTTGTA A A A A G T A G C A A A A A A T T G A G T A T A C T A T A A G T A G A G G A T G T A T A T G A A A A A GGCTATA A A A A G C T C C A A A A
WI-14863	61 G A ---			ATGGCAATTTACTTTATAGCAATGAACAATATTTGTCAAAGGGCAAAATATTTTGTCTG[G/A]AG TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCAC TAT TATTGATTGCCACT ACCTGGC
WI-14867	46 T C A		GACATTCCAA GGCTCTCTAAC	TTTTAATTAACGTAA A A A A G G C A G G A C A T T C C A A G G C T C T A A C A T T C / G A G I G T C T G C A G C C C C A TTCGCTTTGAGATGTGAATGTGTTAACCAGGGTGGA
WI-14733	98 G A A		CCAAATTGAC AGATATTCTGC	ACGGAGTCGTCTCTGATGATTTCTTTGTCAA A A A A A T G T T T G C C T G A T T C T A A T C A T G A A A G A A C A A T T AG A A A A A A T C C A A A T T G A C A G A T A T T C T G C A [G/A] A A T A A A T G G C C T G A C C T C A T C A A A A A C A T C A ATGTCATGA A A A A C A C A A A A
WI-14898b	79 A C ---			TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCICATAAAGGTGCCACTAAGGAAA ACTTCTCCAT[G/A]AAGCTGCCTGCTGTGCACGTTGCCTGGGCTTTGTAAACCCCTGGTGTGCATCT GCCTGTGTTCTGCTT
WI-14898a	50 A C C A		CATGTACAGG AAGAGTTGTCT	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT[G/A]AGGTGCCACTAAGG AAAC T T T C T C C A T A A A G C T G C C T G C T G T G C A C G T T G C C T G G G C T T T G C T A A C C C C T G T G C T C TGCTGTGTTCTGCTT
WI-14907	48 G A		GGCACACATT GGACTCTGAC	TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC[G/A]ATTCCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGGCACACCCCATCAATCAGTGACTCCTGCAC TGCAGAGGGGCCACATG CACGATGCTCAGGTGTG
WI-14911	52 G A C		CCAATACATT CAGTTCCTGGT	CTAGAACTCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCAGTTCTGGT[G/A]AAGGTCTCTTTTC CTGGTTTGCAGACAGATACCTTGTCTGTATCTCTCACATGGCAGAGAAAGAGGAAAGTAATCT
WI-14913	88 C A ---			CTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACAGCAATTC TAGTGATAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTTCATATACAGATCAACCAATCCAAAC CTACACCTCCAACCACT
WI-14914	66 G C A		CTGGACACAG TTTTCTCTAGC	ATTTCCTTGATTGGCTGTCTGTAAGCCCTGTGAAGTCATGCACATCTGGACACAGTTTCTCTAGCA[G/ C]GAATTTATTTGCTCTGGGCTTGATGGCTTTTCACAGC
WI-14926	49 T C ---			GTTTATTTCAAATGACACATCCAGATTGAAATGGGCACCTAGCGAAT/CJACTTGTGGACCACA AGACTGTCTGAGAACATGTTCAAAGACAGTTTTCAAAATAAAATTTTCCCTTAATCAGGTCCA

WI-16083	89	C T	ATGTTTAAACA CAAACATATC AAGGAT	TGGAAAGATT CCAGCCC	GCATCTTTATTACACAGAACTCATTTAIGTCCTTAATCATGTTTAAATATAATATAAAGCATGTT TAACACAAACATATCAAGGATC/TJGGGCTGGAATCTTTTCCATCTATAGAAAAGCACAACCATC CATTAAGGCAG
WI-14930	55	C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTCTGTGTTCTGGAACAGCTCTCCTTTCCACAGGAGGAGTCCCTCATGGATC/TJGGCGTATTG GTTGGTTGTGGTATTGGGAGCACAGGGAGAGCAA
WI-14946	47	T C	---	---	TCAATACTGAAGGTGCAAGTGCTCTATTGGCCCCAGACATAACA/TJCTCTAAATCATCCTCTTA GATCAGGGAGTCATAAGGACCATTAAGGCTCATTAACACAGTACTTTATGGAAGGATT
WI-15987b	80	A G	---	---	ACATTAACACAGCACAAATTAAGGGTCCCAACGAGGTTGGTAGTGCCCTCCACTATGTGAGGACAC TAAGAAGATGGTC/TJCTATGAACCAAGCTGCCGGTGCCATGCTCTTAACCTCTCAGC
WI-15987a	32	C T	CACAAATTAAA GGGTCCCAA	GGAAGGCACTA CCAACCTC	ACATTAACACAGCACAAATTAAGGGTCCCA/TJGAGGTTGGTAGTGCCCTCCACTATGTGAGGA CACTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCATGCTCTTAACCTCTCAGC
WI-14948	56	T C G	AGGGAACTG CTAAGTTGTCA	GATGATCTTAC ATCAGTTGTG	GAATAAAGTTCTTATTGCCGTTCTTCAGGGAACAGGGAAACTGCTAAGTGTGAGTCTCAG/TJCTCCAACA ACTGATGTAAGATCATCTCTGACCATAGCGAACCTGTAAAGGCTTGCTGTTCCCTCCAGCTGA
WI-16100	52	A G	TTGA	ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAGCTATTTTCTACACTTGAC/TJGTAATATACTG TTTTCTGACATCTCTTATCAACTCCTCTGAAAATC
WI-14958	83	A G	CAAGGG	TTGGGTTTT	GTGATTGATCTGTAATATTGGGATTATTTATCAACTCTAAAATTCGAAGATGAAAATAATTTATCT CTTCTCTTCAAGGG/TJGAAAAACCAAAATGAATGCAATTTTCAAGTTCTCCAGGCCCTTTGAAGTGC AGCAGAAAATTCAGGA
WI-14976	35	C T	GTGATTGCT TCGTTCAAAG	TCAAACATAAT CTTCCATTCTA AGC	TATTTTTTAATTGGTTGATTGCTTCGTCAAAG/TJGCTTAGAATGGAAGATTTAGTTTGAGGAG GGGAGGTTTGGGGTAGGCTCAGCGGGCATAGTGGCCACAAAGAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACTCG
WI-14981	31	G T	TCAGTGGTGT TATTGGATTT	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTCAAGTGGTGTATTGGATT/TJG/TJTTATGCTAAGTATTATGTACAGAGGTGGAGAT AAAGAGGAAAAAGAAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80	C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCCT	TGATTACATTTTTTAAATCATGCTACCAGCCCATCTAAGCCAAATTCAAACACCACCTCTGCATTA AATGAAGCTGCAG/TJAGGAAAGCTGAGCACATAGCACCCTAAGTATCGGAAAGAAAACGTA
WI-15002	72	T A	---	---	AAATCTCTCTTTCACACACAGATGAACCTTTAATAATTACAAATGCACCTGAAAATGCCTTCTTGA TTTCC/TJATTCAGTTTAGCCCTCAATGGGCTCTCCTCAAGGCTGGACCTCAAGGCCAGTT
WI-15000	90	G A	GACAGAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTA/TJG/TJGAAAGTTTGTGCAGAACTAGAAAACAAAAATCCACCT

WI-12323	68	G A	CACAATACTT CATGTACCTAT GAAATAA	CACTGGACATA TTCCCTACCTG	ATTTTGTGATGTTGTTAAATCTTATCTCTTTTATACACAATACTTCACTGTACCTATGAAATAA G/AJACAGGTAGGGAATATGTCAGTGCAAAACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91	A T	AAGGACGAT TTAGTATCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTATTCACGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTAGTATCTAAAAACA/AJTCAAAAAAACACTGGGACATGCCOCTGAATTGCAAGT TGGAGTTCGTAAAGATCTAC
WI-13470	100	C A T	CCTGCCCTTAT ATTGGAATTC	GGGAGACCATG GGTCTCT	ATTTTGTGTTTATTTAGCACCTGAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCCTTATATTGGAATTTCTA/C/AJAGAGACCCATGGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGOCCCTC
WI-14712	38	T A CA	TGAATGCTTCC AAGTACAAAT	TGAAAGTATGT TGTATATGGTA TTGTA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAATCA/AJCTACAATACCATATACAACATACT TTCAATCACAACCTCAAAATATAAAATAACCTACAAAATCACAATTGC
WI-13712	40	A C TCTATTG	TTTACTTTGTT GTCAATTTTAT	CCATAAGGTCT CACACTTTTCT TAT	TGGGATACCCCTTTACTTTTGTGTCATTTTATTTCTATTG/AJCTATTATAAGAAAAAGTGTGAGACCTT ATGGCTCTGCTTATTTGGCAATATGCAATATAATTTGTGTTGTTAAAAATTTATGCAT
WI-16163	35	C T A	TCTGGTGATGC AATTGAAATA	GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTTACTCTGTGTGATGCAATTGAAATAA/CJATTGTAAGTTAATGTAATTGGCAGCATT GCCCAAAGTTTAAGAGGACTATTTCTTTAAACAAAGACAGTGTGACATTTATTTTCAGGT
WI-13453	88	T A TC	AATGCACAAA ATCTTGCTCT	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTTGCAATTTGAGTGTCTTATTATATTGGGAATTTGCAAGTATTAACATTGTGACAAAT GCACAAAATCTTGCTCTCTC/T/AJTGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACCTCATTGTCCAT
WI-16167	58	T C GATTTT	CGCACTCTAA ATTAGAGATA	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTCTGATATACATTTT/CJCATCTT ATTCACCACGAGCACACACCGCACAGTAGAACAGTTCCACACCTGATAAAATTGCACAAGATG
WI-14482	17	G A ---		---	GCAGAACCAATTAAATAA/G/AJATCTGCAAGTTTTCCCAAGAAACTCTGGAAACCATAGTGCCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGAAATAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T C ---		---	TGTAGTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATACTATGTGATTTCCAGTATCATGTAC GCACTAAAAAAAAT/CJGTGTGCTGTGCTGCTGTGAGTGAOCCATTGCTTAAGATAAA
WI-16156	97	A C CCAGAGTCGC	TGAAGATTAA CCAGAGTCGC	AATTGTGIGA TTTTGAAGAGA	ATCTGGTATTTGIGTATCCCAACAAGTATACAGAACTCTATAAAAAACCAACCCCAACCCCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTCGC/AJCTCTTCAAAAATGCACACAATTAAGACG
WI-15012	59	G T ATGT	GCAGCAAGAT TACATCAGTA	CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATATAATACAGCTTTTTTTCATTGAAGCTTTTGTATTACCT TACTATACTCTAGGCTATTTGGAGTGTCCCCAC



WI-15100	74 G A ---			TCCTATTACAGGCCAAGAAAAATACCCAAATTATTTCCAAATAAAGCAAAAAATTGGAACAGACTGGA GTGAGAAQ[G/A]GGTTCCACCACCAAGCCCCCTCAAGACAAGATGGACACGGCAGCTGGTTCTGGGGT GCATTTCTAGTGGACTTTAT
WI-14492	92 A T AATTACT		CCTTTATTTTC CCAAATATAA TAAGAC	TGGTACAGAATGTTTAATTACAGCAGGCGAGTGATTCAGTTAAATAAAATTAATAAAACCTTTATTTT CCCAAAATATAAAATTAATAATTAA[A/T]GTCTTAAAGAAAATATAACATGGTGACAGCTTT TCCTTAATTTTATCGGAATCCAGGACACAAAGAAAAACACCCAAAAACCATGGAGACAGAAG ACGAGACACAACCTCCTCCCCAC[T/C]GCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGTGAGAC AG
WI-12002c	89 T C ---		---	TCCTTAATTTTATCGGAATCCAGGACACAAAGAAAAACACCCAAAAACCATGGAGACAGAAG AC[G/A]GACACAACCTCCTCCCCACCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGTGAGAC AG
WI-12002b	68 G A ---		---	TCCTTAATTTTATCGGAATCCAGGACACAA[C/G]AAGAAAAACACCCAAAAACCATGGAGACAG AAGACGAGACACAACCTCCTCCCCACCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGTGAGAC AG
WI-12002a	30 C G GGACACAA		TCGGAATCCA GGAGCCCTA GTTGCAGTAA	TTTTCAATTTATTTCCAGAAAAAGAAATCACATTTTCAGTAACAACTTACATATAGAAATTAACCTTTG TTC TGAATGGAGCCCTAGTTGCAGTAA[C/T]GTGTCAATAATAATAATTGCATATTCAGGATTTTG TGAATAGGTGATTGGGA
WI-15116	96 C T GTTGCAGTAA		ATGACA	GCAAAAGCAAGCTATGGAGCCCTAAAGGAATGGAA[C/T]GTGTGGTGGCGCTTGATACCTTGGT GCTTGTGTGCATGGAGCAGAGTCTTCTGGTCCATGCAGGGCGTCACATAATTTAACTGCACATAAT TTGGCNAACCTGTCATTC
WI-12578	37 C T AATGGGAA		TCAAGCGACCA CCAACAC	ATTTACAGTTGGCCCAAGATCTCCCTTATGTGGCATTGCA[A/G]AGACACTGCACCTTATCTGAGGTTA GAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATACCATTTCCCTAA
WI-15153	40 A G GCATTGCA		TGGCTTTAGAA TCAAAATGGG AAAAGTCA	CCTTGTCTCTGAACTGGGACAGGATGTGAATAATTTTGAATCTGATGCAGGTGAGGTATGGC TTTGAATCAAAATGGG[G/C]TGACCTTTTCCCTGTGGTGGAAAACTCTGTGAGGGTTGGCA
WI-15215	84 G C TCAAAATGGG		CTTGAGGACCT AGAAAGCAAA TAATCACTCC	AGGAAAAGAGTGGTAAAGCAAGGCGATCATTTGGATGGAATGATTATGTGTACGAGCACTTGAGGAC CTAGAAAAGCAAA[C/T]GGAGTGATTATGCCAATCAAAATGCAAGGTGGAGATATGCTAAAA
WI-15225	80 C T C		---	AAATTTGCTAGTGCAAAATGGACCAGAAATTTGGAAGGGCTATGTAACCTACACA[G/A]TATGCACACCAC AGCCATGTCAAGTGTACAGATCCTCTTGTGCTTCTTCTTAAACACATCAAAAGGCTGCA
WI-15152	51 G A ---		---	TGACTGTATACCAAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCCTTAAGCAATTTACAACCTCACTGGGGAAGAAACAGACATGCAACACAGATAAACACAAT
WI-15123	55 C T TAGGATG		TGTTAGTGACA GACAGATAAA CAACACAGAC	

WI-15182	49 C A	GCACAACAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACACTAGCTAGCTGCACAACACGAGGCGCAAAATA[C]/AT/GCTGGATTAACCC ATGCTAATGGGTTACCTTTATTTAGTAATCATGGTCCCTCATAGCATGGTCCAGATCCG
WI-15198	38 T C	GGGCGCTGGC ACTATG	ACTTATCCGTC AGGCAGAGTAG	GTGGACCTCTACAAGTACCATGGGCCCTTGGCACTATG[C]/CTACTCTGCCTGACGGATAAGTTGGC ATATGGTTCCAGATTGCTTGTCTACACAGTCCAGTTTCCCTAGAGACTAGTCCGACTCTCT
WI-12601	42 T C	TGAT TGCAAAATA	GTGTAGTCTT ACATGCTTACG TAGAC	TCAAGTGGTAAATAGCCATTTATTGAGTATTCCTGCTTGTGAT[C]/GCTACGTAAAGCATGTAAGACT ACAACTTACGACCCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAACAAATTTTGTCAATTCAGAT T
WI-14510	104 A T	TGCATAACAA TAA	TTGAAAATGGT TAACTGGCA	ATGTTGAGAGTAATAATGCCCTACATATTTAGTGTAGTACACCCACAGATATTTTGGGAGAAGAG TTGTTTGTCTTTTGGGCAAAATATGCATAACAAAAT[A]/TGGCAGTTTAAACATTTTCAAGAGT
WI-15239	57 T C	CAATTGCAAT AAACACCATC CA	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAGATTGTGCATTTTGCATTAACAAACACCATCAT[C]/CCTGAG TCCACAGATAAGGTCCCGGAGAGGGGCTTCCCTCCTCTCTCGCTGGTTGACGTTCCCGAGCGAGT GAAGCCTTTCTGGAATG
WI-12634	52 T C	GCATCATATG AAGTGTCTAGC AGT	GGACAAAATTGT AAACATAGCT AATAGC	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACCTGTCTAGCAGTATTAT[C]/GCTATTAGCTA TGTTTACAAATTTGCTCGAAGGGGTCTAGATGTACACCCAGAAAGTGGTATTCTCTGA
WI-15249	34 T C	AAAGTTCTAA AAGACACCGT GCAATGC	GGAAAGCCAG AGATTTTAAAC AA	TTTGCTGAAGGGCTTGACACAAAGTTCTAACTTT[C]/TGTAAATCTCTGGCTTCCCTGGCTGG TGAGGAGCAGAGGTGGGTCTTCAGGTATCCACTGGTGGCCCGCATCTGTCCCTCCACTCCCGAG CCACATCTCTGGCTCT
WI-12159	28 C T	AAGACACCGT GCAATGC	CCCTCTCCTCA GTGCACITT	CTGTCCGGGGAAGACACCGTGCATAATGC[C]/AAAGTGCACCTGAGGAGAGGGGGTCTGTGACTC CCAAACCCCTCGAATATTTTATGAATCTAAGAGTCCAGACGCGATTCATCCACGGAGATCTGC
WI-12648	41 A G	OCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC T	TCCCCAGATTGTATGGAATGCCCTAGTGGCATTAAAGGATGC[C]/GTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACCTACTCCATGTTAGGTGCTTTACTTGGATTATCTCACTTAAACACACA
WI-12684	64 G T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTTCAGTAAACCATGCTGTAAACAGCTGTGC[C]/ TCCATTTAGGCTTTGTTGTTCCATTTAGAGAGGCACAGGAGGAAATTTAGCATAATCTT
WI-15260	75 G A	AAAGGATGAA GCTAATCATG GA	TCCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGGTGCACACAGCGGACACTGTCTAAGTGGAAACAAGGATGAAGCT AATCATGGA[C]/GCAAGCTCCCTGGAGAGACAGGACAAAATCAAGATGAGCTGGAGAAATTA TCCTG
WI-15325	39 T C	CATGTGGCTGG GAGGC	CCTTCCACCAT GATTGTA	AAGGTTTAAATGGACTCACAGTTCCATGTGGCTGGAGGCT[C]/TCAACAATCATGTGTGGAAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC
WI-13936	123 C T C	AGTTGGCATTC AATAGCCTAT	TGAAACTCCCA CATGGAGTT	TATTTAGTATTTCCATGGCGCTTCTCACTCCCTATACATTTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTCAAGAACCTATGACCTGTATCTTCAGTTGGCAATCAATAGCCTATC[C]/AACTCCATGT GGGAGTTTCATAATAA

WI-14528	62	T G	TTTAACTTTT TCTGGATGGTA TAAAT	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTAAATATTTTAACTTTTCTGGATGGTATAAAATTT/GTT GAATTATAAATTTTAAATTTTATAATAAGTCTAATCGAGACATCACCTGGGATATAATTGA
WI-15347	74	C T	GACTCAAAG GAAAAGAACA AATTT	TCACCTCCCCA AGCTTTTG	TATTTCTTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTTC/JCAAAGACTTGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA GG
WI-14546	95	C A	CCAATTTCTAG TGATAGTAGA GGACTCA	AAGGTGCACGT GCAGG	GTAATTTCTGATGCTTTGACATCTGGGGCATTTGCTGTCTAGAGAGACTACTTCTCTGGGACCAGC CAATTTCTAGTAGTAGAGGACTCA/C/JCCTGCACGTGCACCTTTCATATACAGATCA
WI-15353	37	G A	---	---	TTTATGGCTGTCTGTAAACAATGTGGTGAAC[C/GA/JCTTAAATCAGGACATCTCCACCTTG TTTGGCTTCCAGTTGTAAGACCAAGTGTGAGGCACATAGGCTGATTATCAGTGG
WI-14580	100	G A	CATCCCATCT GTCITGCA	CCGACCAAGAT COCTCC	AGAAATTTTTCCTTTTAAACAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAAAATAC CTAGTTATTATACACATTCCTCATCTGTCTTGCA[G/A/JGGAGGGATCTTGGTGGCTTAAACA
WI-8540	73	T C	GGCTGCATTT GGCTTA	GGCTTCTTTT TCAGGCAC	CCAGCTGGAGGTGAATAAATGGGGCAACCAACAGAAAAAACACACAGCTACACACAGGCCTGCATT TGGCTTAT/C/JGTGCTGAAAAAGAGGGCCGACCTCTTGATAAAGAATGTCT
WI-8039b	97	T C	---	---	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAAATGCACACTCGCACATCACGAGTAAATACTG TTTGGTAAAACTTTGTTTCAGTT/C/JAAATATGTATGTGTCCTGGCATGTGATTAATATCTTCT TACCAGTCACTCCCTAAAGAACCAAGCTTAGGACTAGGGACACAACTATGCAGAAAGAGCAGGGA GACCAGACACTCTGGTTGAGATGATGATTTTAAATGCCGAGCCGACACCCACA
WI-8039a	87	T C	---	---	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAAATGCACACTCGCACATCACGAGTAAATACTG TTTGGTAAAACTTTGTTTCAGTT/C/JAAATATGTATGTGTCCTGGCATGTGATTAATATCTTCT TACCAGTCACTCCCTAAAGAACCAAGCTTAGGACTAGGGACACAACTATGCAGAAAGAGCAGGGA GACCAGACACTCTGGTTGAGATGATGATTTTAAATGCCGAGCCGACACCCACA
WI-8044	107	C A	---	---	CACAACATTCAGAAATTTCTGCAATTTCTGCTCTCTGATGCTAAAAAGATTTGAGCTTTGACTAT ACGATTTCCACACTGAACGCAATTCATAAGGTTTCTCC[C/A/JAGTATGGATTTCTGATGATTAATA AGCCCCGAATCTGGCTAAAGGCTTCCACATTCAGACATTTGTAAAGTTTTCTCCAGTGTGGAC TCTCTGGTTGCAAGAATGGAACCTCGGCTGAATGCTTCCACACT
WI-8550	32	G A	GGGAACATCA ATGCAACAAG	AGTTTACAAAT T	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A/JAATTTGTAACTCAAGCCACAACATTAGTTA ATAATCATGGTTAAGGGACATTTGCCAAAGAGCAACTGATGCCTCAGTGAA
WI-8057	87	T A	---	---	TATTAGATAAAACCCCTTTGTTCCCGATTCCAGGATGTTTAAATTTGCTTCTTTAACTCTGTGACTTTT CCTGGTTCAAAGGACAGT[A/JAGTGGACAGCAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTCTGTGGCTCACAACCTGCCCTGTGAGAGGATGCTGCCTTCCAGGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG

[illegible]

WI-6375	28 A	GGTTATTGCA TATGGAATC	AATGTGAGATC TTTATTCTAAC CTTTT	AAGGTTATTGCATATGAAATCAATAG[A/G]TATCTTTTACAAAAAAGGTTAGAATAAGATCTC ACATTTGTAAAGGCACATATGAAACATTTTATAGCAAGCACAGGCGAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTCTGATAAGACAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA[T/A]GCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T	A ---	---	TTGTGCTCAACAGATGAAATTCATAACCTTGTCTGATAAGACAATTCAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A	T ---	---	CTAATATAATCCTGGGCACATGGATTCCAAAGAGAGATTTGCAGCAGATTTTATTATAGTTACTTAA CAGCTAAATAATAAGGGTGATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G/T]ATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165 G	T GCTG	AGATGCTTAGG GAAGGTTGATA	TCCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGGAACAGGAAGATGGGC TCCTGGAGTCCAAACAGGATGTGGACGTCCTGGTAGTCTCTCTTTTACACAACCTTTCCCTGAGA ACTGTCCAGTCAAGTGAGCTTCAACAACACGACGCTAAACTCTGAGAGAAAAAC[C/G]CTG ACTTTAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C	G ---	---	ATTGTAATTAATAATTACATGGGCCTATTATTAAAGGACATTTGTAATGTTTCCACCTTGTGTTTAAA [C/T]AATTAACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAAGTTTGAAAAATGGCG
WI-6558b	68 C	T ---	---	ATTGTAATTAATAATTACATGGGCCTATTATTAAAGGACATTTGTAATGTTTCCACCTTGTGTTT AAACAAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAAGTTTGAAAAATGGCG
WI-6558a	42 G	C ---	---	AACCAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAAA AGTTGTCATA[T/C]AGCAATGGATGCTGTGTCAGAACATCTGCCAATAAACCTTTAAGAAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCGGATGTAAAGAGTTAATGGAAGAT ATCGTGAGCCAAAAAC
WI-6629	75 T	C GTCATA	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATCAAACTCCAGCTGTTCTCTGTGCTTT TTACTTAGCAAGGAAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCAATTTCTCAAGCACAT T/C]ACCCAACTTGAAGGTGATTGAACCCAAATAATGGTGGGAAACACCAAAATGAGGTGAGGA ATGAGAAAGATGTGTGGGCCAAAGCTATCTGTTATATTTGATGTTGCCAAT
WI-6644	134 T	C ---	---	TGCTAAACACCCACCATTAATTAAGGAGAGTACTAGGAAAACTACCAACACAGCATGTGAAACAGT TGGGCACGGTGGTAAAGGGCACAGACTCTGGAGCCACAGC[C/T]GGCTAATACACTGCAATATTTTA TGTTTAGCAAAATTATAGCTGGTCTGTGTATACCAGAGAGCGGTACTGG
WI-6690b	106 C	T AGCCACAGC	ACATAAAATA TTGCAGTGTAT TAGCC	

WI-6690a	28 T C	AAACACCACC ATTATTAAGG AGAG	GCCTGTTTGG TAGTTTTCTT CT	TGCTAAACACCACCATTATTAAAGGAGGTC(C)ACTAGGAAAACTACCAACACAGCATGTGAAAC AGTTGGGACGGTGGTAAAGGGACAGACTCTGGAGCCACAGCCGGCTAATACACTGCAATATTTTA TGTTTAGCAATATATAGCTGGTCTGTGTATAACCAGAGAGGGGTATCTGG
WI-6770	53 A G	CAACCCCAA AACATCACA	GCTTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTAAATGACACAGATCTTCCAAAGTAATCCAAACCCCAAAACATCACA(A/G)AATATTTCAT ACTATTATACACTCCAAAGCAAAATACTTCAACTGCAATCC
WI-6686	151 A G A	GCAATCTTCCA AAACAAAAGA	CCTTGTAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTTGAGCAAAATCAGTAGGACTAATCTTGACCAATGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTTTAATTTAGATGAAATTCACATTTAAACATGGTAAGTCCAAAGCATTTCT TCCAAAACAAAGAAT(A/G)AACATTGGAATAGTCACITACAAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGAAATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGCGAGATCTAACAGCTGCAGAAATGG(C/A)CTTCTCCTCCAGCTTTTGTGAACAAAAC AATCTCCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGTTGTCAGGTACAAGGCTC
WI-6824	225 T C	...	...	TAAATACTGCCAACTAGCATTACGTCCTCTTGCATCATTAAAAACAAAGGGTATTTCCCTCCTTG GTATTTTCAATGATGCATTATACAATAAACGAAGTTAGAACTTAAATGCACCTGATTAATATG TAACTGGTAATTTGTTTAAAGCATATAATTTGGTTCTTCTCATAAATGGAAATTTAAA TATTTCTCTGATAGCTTGAGGTT(C)ATCATTATGAGTAGTGCAAGGTG
WI-6889	139 T C AATC	GAAAAATGAG ATGCAGTTAA	TCACITTTGTGG CTTTTAATTTAT TCT	CGGTTTGTCTACACTTAATGGGTTTTTTTTTAAGGGATTTTTTTCAGGCTTGTGACAAACATCAA ACAAAAGGTACTGAGTACTCCACAGGGTACAGAGTGTGCCAA(A/G)CACCTTAGAAAAATTTACAT GACACGGAGAAATGCGCTCTTGTCTCCTTGAAGAGCTTACAGTCTAGGGATTTGACAACTCACAGT CTTAGGAACTGGGCAAGTAAGGCAAAATCTTCCCTCCTAGAGCTATTGTG
WI-6911	216 T C	...	...	GTACAAAAAGCTGAGAAGAGCCCAACATGGAAGTGTCAAGAAAAACATCTGATAGGTACGGACAA AAGAGCTCCTTCAATCAATCAAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC(T/C)JAGAATAATTAAAGCCACAAAGTGAAACTGTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-9413	112 G C	...	...	TCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACCTCAATATCTGATGAACCTGAACTGAA AAGAGGTCTCCTTAAACAAGATATCATCTCCCGAAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCAGAAAACCTTGGCTTCCCAAGGAATGTGTTCTAATTTGGTTTCAAGCACACTGGTTCC CACTTTTACCAC(TT/C)CATGACATTTGGACAATAGTACTCTTTTCTAC
WI-9557	74 C T	...	...	GCCAGTCTCTAGTAAGTCTAGGGACATGACCAGACAGAGCCCTGTTCTATATGAAGACAAAAC AGGTGGCCATACTTGGGTGAGGGATACCGCTGCTATTTCCAGATG(C)AAGATTTGGTGAAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCAAAAACAGAGGTATGA AAAAAGCTTTAAAAAAAAGTGGTGTCTATCTTTAGAAAACACTTTACGCAAGATCAAGTAGCCAGCT ACAGCC(TC/T)GGTGCATCTTAACCCCTCTCCTTTT

WI-9617	37	G T ---	---		TGCTCTTTTATTTACAGTTCACAACACACGCCGTG[G/T]GGCACAGTCTACCAAAGTGCCCGCAG CGCCACGCTTGGCCGGAAGTCTCATCTGTCGTCTCTATGGACTGATGAATTTGGGATGGCCAG CTCCAGAATGTTCCACGTGGGGCACTCTGTGGCAGAGAGGCTGAGCCCTTGCCCCACACTGGCACCA AAGAGTTGCACGATGCAGCTGCAGTGGGTCGAAGCCGGGTGCTGTG
WI-9657	121	T G ---	---		AATGCTGGAGAAAACATCAACATTGAGTTGACATTTGTTTTGCTGAAATATAGCTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAAGCCAGATTCTCAAAATAAAGT[G/G]ATAATCTT TGTAATAAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTTTAAAAAAGTAAAAA TTTTAGACATATGACGCTTTTCATAATTAATGCTTTTGATATAGATTTGAGG
WI-13119b	114	G C GCTGGGA	CCTCCCAAGTA T	AAAAATTAAAC CAGGTGTGGTG	CAGGCTTGCTGCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT[G/C]ACACCACACCTGGTTAA TTTTTTAATTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAAAACCACTAAG CAGGCTTGCTGCTCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT[G/C]ACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTA ATTTTTTAATTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAAAACCACTAA C
WI-13119a	51	C G ---	---		ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT[C/T]CTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAAGAAAATATAAATAGT TTCAGTATGTTATGATAGATCACATACTATGGCAAAAATATTTTATTATTTGAGGGAATAGGCCAAT TT
WI-13112	71	C T AGCTTTT	TTAGAAATTTT GTGTATTATAT GGAAAAAG		TGTTAACATTTTATTTGGTACGTGCTCTCAGTACAA[C/A]AACAGCATCAGTAGTGACACTTTGAT AAAAAGGAATTTTATAGCTTAGTAGAAAAGAAAGCCCAAGGTCAGAAATATAATGAATATGTACAT CTTTATGGAAGTCTTTGTGTGACCATCTTTATCTTCCCTGTGGATGAGATGATGACACACAAAGT AAA
WI-12988	36	C A CTCAGTACAA	TGTTACGTGCT CTACTGATGCT GTTT	CAAAAGTGTACA	TGCTATTCATGACAGACACGTGAGACAAAATATCTTATTTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGAACCCCTGAGACTTTA[G/A]ATCTGCAAGGGGTTTAAATAT GCAATATCACATATATTTCCATTTTAAACACCATATTAAGTTTCCATTTTCTTAATAGAAAATGA TAAAAATGTTTTCCCAATAT
WI-13020a	108	G A CTTT	CAATTATTAAAC CCCTTTCGAGA		TGTATAAAAAATCCAACCTGTTCCACAAGTACATATGCTTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA[G/G]TACAAAAAACAGCAATTTCCCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAAGCA AGTTGTGTCCA
WI-12837	87	A GAAAGTCCA	CCATATACAT ATATCAAGGT GCCATAGGAA ATGCTGTTTTT		

L42611b	50 GC ---			GTCTCAGGCCCTCTCTGGCTGCAGAGCGGTCTCTCAGGTTGCCTGTG/CJCTCCCTGGCCCTCTAG TCTTCCCTGTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGGCCCTCAGCTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATATGATTCACCA CTGGAGCTTCACCTTTGTTAC
L42611	34 TC ---			GTCTCAGGCCCTCTCTGGCTGCAGAGCGGTCTCTCAGGTTGCCTGTGTCCTCTGGCCCTCTAG TCTTCCCTGTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGGCCCTCAGCTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATATGATTCACCA CTGGAGCTTCACCTTTGTTAC
WI-1172b	179 C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG	TGAACGTGTGGTTAAACTAGGCAATTGGTTAAATCAATTTAAACACAGGCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCAGCTCAGATTATGTTCTTGAATACCATTTCTGCTTTC AAAAGAAAGACATGAGGCTCTTGAAGAAATGGCTGATACCAAG[C/T]CTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17 C A ---			TGAACGTGTGGTTAAAC[C/A]TAGGCAATTGGTTAAATCAATTTAAACACAGGCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCAGCTCAGATTATGTTCTTGAATACCATTTCTGCT TTCAAAAGAAAGACATGAGGCTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35 G C A	GCAGATTGGA AGTGTGAAAA	CACCTACATTT CTGAATATTTA GACTCTTT	AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTTCAG AAATGTAAAGTGTGCCCCCACTGTTCTTTACCCCACTTAATTCGCAATTTTGAAGAACTAGATTGAAT TCCTTTGCAAAACCCCTTGATCATGGATACCCGAGTTAAACCGTTAATTAAGAGACATTTAAACATGG CCTGGTG
WI-1231b	141 G A ---			TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCGCCATATTC CAACTAAGCAGGAGGTTCACAATAAACAACATAGGCTCTTTATTCCTCTTTCATTAATTTCTT TCAC[G/A]TTATCCCTCACCCCTGAACGCCCTTCTTCCCTCGTAGTGACATTTTAAATCCACCTTAC ACATTCGGACC
WI-1231a	126 T C A	GGCTCTTTATT CTCCTTCTTTTC	CGTTCAGGGTG AGGGAATAA	TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCGCCATATTC CAACTAAGCAGGAGGTTCACAATAAACAACATAGGCTCTTTATTCCTCTTTCATTAATTTCTT CTTTCACGTTATCCCTCACCCCTGAACGCCCTTCTTCCCTCGTAGTGACATTTTAAATCCACCTTACA CATTCGGACC
WI-472	114 G C ACAGAAAAAG	ACATACATAT CCATTATACA	GACCTTTCTTT TCCAGGCC	GAAAGCAGGACTGTGTTTTGGAGGACAAAAAGTAAATCTTTTATATCTTTATTTTTTAATTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACAACAGAAAAAG[G/C]GGGCTGGAAAAAG GTCAAGTGAGATTTCAGATATTCCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT



WI-478	46 C	GCATGCTGTG TTACTCTATTT TGITC	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGCTGIGTGTACTCTAATTTGTTCTC/TJAGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATACTGCTTTAAACACAAATAGAAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAAAACCAAC ACTGCCCA
WI-533	29 T	ATCACAGCAG AGTACCTTTCT AACT	CTTCCAACTT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTCTAACTT/C/JATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGA CTGTTCTGTTGGTATAATGACCCCTGTGTCCAGTTAATCCA
WI-601b	112 T	---	---	TCACCTATCTCTTTTTTTGGTGAGAACACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGCGGAACAGAGAGGTTTTCATTGACTCCTAACTGAGTAC/T/A/CAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C	---	---	TCACCTATCTCTTTTTTTGGTGAGAACACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGC/TJGAACAGAGAGGTTTTCATTGACTCCTAACTGAGTACTCAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAAACAGACACCCCTCGGCTTCTTCTCACAGTCCACATGGGTGCCAAACAATCCACATTCCT ACATCTCCTCCCACTGGCTGCCCTTCCACAACCTCACCA/JA/GIACTTGGCTTACCGGGAAGCATAAA GCCAAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36 G	ACTGCTTGCTT GTTGATTTAAT C	TTATTCTAATC CCACATGACAG C	ACTCACTGCTTGCTTGTTGATTTAATCAACCTAGCC/GA/GCTGTGCTATGTGGGATTAGATAAAATA AACACAAAAATGAAAAACACACGATTGCTAACAAAGCAGATCTTTTTCGAAGGCACACGTAAGAT AATAACTTCA
WI-991	37 A	---	---	TGCATTCTATTATGCACCAATAATAACTTCTGTACAT/TJ/CATTATTGTTATTTTATTATCACAAAAAT TATGATGAGGGATGATTGTTATCCCTATTTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCAAAGTCACAAAGTTAGTGACAGAGCCGGGATTCGAATCCATCACTTGAATCCAGAGAAAAAT GTTCTGCATCACTGTACACACTGACTCCTTTTCTCCTTTGAAACAAGGC
WI-1011	70 G	CAGTATCTGA AGTTTTTGTCT CCA	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTTGCAGTGGATACTGTTTGAAGGCTGTCTCAGTATCTGAAGTTTTTGTCTCC A/GC/JAGAAGTCAATTTGTAGGTGTTCTGGCGTTTTTGTACGTTTCCATTTTCTTAATACACTGC CGTCTTAAGGGAGGCTTGCAGAGCAITTAACAGATGGCTGTTTGTGCTGCACTGTGCACTGAAG
WI-5381	178 A	---	---	TTTCATGCAGAAAGGTCCTAGTTTACAGATCTCAAGGAAGAAAGGCCCTAGAGATGACACCCAGAA ATGAGAGTGGCTTGTCTCATGAAAATTGGACAGCATGTTCCAAAGCAGAGGGAACAGCATGGAGAAGA AAAAATCATCTATCCACGTGCAGAAACTGGCAATAGTTTTGT/TJ/TACTAAAAACACAAATGT TTAACTTGGGGTCCACAACAAGGATATGTTGGCAATGGTATTCTGTGATG
WI-5791b	76 G	---	---	CTATGTAATTCCTATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCAAAAGATGAGAACAGGTCCTA GAACCTCAG/G/JATCGAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCAAAAGGTA AAAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTCTTATTTTGGCCACCCTGTTTGT TAGGAA

WI-5791a	44 C G ---				CTATGTTATCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTTC/GIACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCCAAAAGGTA AAAAAATAAAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTGCCACCCCTGTTTGT TAGGAA
WI-5406c	120 C T ---				CACCTGCTGTTGTCCATGGGTGCCACAGACTCTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/TJATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGAATCTGTGAAGAGGAAGGAAAGGAAAGGAAAGAGAGGCAA GG
WI-5406b	118 C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAAGT GTGGGCTCAT		CACCTGCTGTTGTCCATGGGTGCCACAGACTCTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/TJATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGAATCTGTGAAGAGGAAGGAAAGGAAAGGAAAGAGAGGCAA GG
WI-5406a	42 A G ---				CACCTGCTGTTGTCCATGGGTGCCACAGACTCTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC GCTTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGAATCTGTGAAGAGGAAGGAAAGGAAAGGAAAGAGAGGCAA GG
WI-5798	48 G C TG	TTTATCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCGATATTTT TCAAT		CCATTCCTTCTTCCCTCCCTTATTCCTCCCTTGTTCCTTTTG/GC/JATTGAAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACATGTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54 T A TTT	TCCTCATGAAT TCATCTTTCAG	GGACTAATTCA TGATCCGATCT		CCTGCTAATAATAATTAAAGCAGCAI TTGCTTCATGAATTCATCTTCAGTTT/T/JATAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41 C T G	TCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG		TGTTTTAACCCAGGCAGACCTCCAGAGAAAAATCCAAAG[C/T]CTTAAACCATAATTTTGTGTTTA GAAACTCCTGTGCCAACCCACTCTTGATGTGAGTGAC
WI-5481b	131 A G CTGCAGTCG	TGTCATTATG CTGCAGTCG	TTACTTCCAGG CTCCAAGTATT		AAGCCAAATTCACATTAGTTGATGAATTTGAAATTTTACAGTATCTAATGCATGGGCATCTGTTCAAC TCCTGTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCG[A/G]A ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
WI-5481a	29 G A AATTT	CCAATTTAC ATTAGTTGATG	CCCATGCATTA GATACTGTAAA ATT		AAGCCAAATTCACATTAGTTGATGAATTTG/AJAATTTTACAGTATCTAATGCATGGGCATCTGTTTC AACTCTGTTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCAATTTATGCTGCAGTCGAA ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
WI-5492	38 T C ---				TCATGAGCTTTCTTCAAGATGCTTGTAAAGTCCCAT/C/CAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

WI-5826	134 T C ---	CCCAATACTTT TTCAGGTGAA	---	TATTTT TTTTCTCAATTCTGGAGCACACCATGCTCTTCTATTTTCATGCTTCACATTTATTTT TTTCACCTAGTTAAATGCTTTTCCCTTGATGCAATGGCCAGTTTATACATATTTCTTTAGTC/C TTTCAAAATTAATGCCACATAGAAATAATTTTCTAACCAACAGCCAAACAGCCTCACTCTTCCTT CCTGGTGCAATTTACTCTTTACAC
WI-5546	40 C T A	TTCAGGTGAA	CCTGTATTTTA GCAACATGGG	CCTTATAACCCAACTCTTTTCAGGTGAAANAAGGGAAC/C/TACCCCATGTTTGCTAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGAATTCGTGATGTTGGGAATAT TAGAANAATTAAGCGAGAGAGGCA
WI-5552	97 C T TTTTAGAGT	GGCACAGGCT	TGCACAAATTG CCAGG	TGTTGTCTGACCTCCCAACAAGTGGTCAATGAGCCTCAAGGTTTGTGAGCGGGTATGGGT GGGGCTATCGGCACAGGCTTTTTAGAGTC/TTCCTGGCAATTTGTCAGTGTGTCAGA
WI-5836b	161 C T ---	---	---	TAAGTTGATTTAAACACTCTGTGCCCTCAATTTCTCACCTATAAAATAAGATAATAGTATCTAAAA AAAAGAGAGAGAAATTAAGTGGATAGACATGAATAACTGTGATGATCTGTTGTATCCCTGAA TCCTGCAATATACACATGATTCATGAT/C/TCCATTTTGAAATTAAGCTTTTGTGAATTTGTTTCCA ATG
WI-557	58 C T AGTGGGA	GTTCAATAGG	TGAACAGTTGG AGAGTAATGTG TC	TCGGGTATTAGGATGGTTCAACCTCGATGATGATGGCGTTTATAAGGAGGTGGGA/C/TGACAC ATTACTCTCAACTGTTCAATCAGAACACTTCACAGCG
WI-5850b	134 G A ---	---	---	CAGGACCTTGGAGCCTTTGCTGTTTGTCTTCCACCCCTCACTCTTCTGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCCCTATGACACGGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTC/GA TTTTGGCATTTCCTGTATATCAACACAGAGAGAGAGGGTGG
WI-5850a	92 C T ---	---	---	CAGGACCTTGGAGCCTTTGCTGTTTGTCTTCCACCCCTCACTCTTCTGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCCCTATGCA/C/TJCGGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCCTGTATATCAACACAGAGAGAGGGTGG
WI-5612b	125 A T TTC	CTATTAAATGA GCATCGTGTCA	TTCTCTTGAGA AACCTAAAAC ACTG	TGCCGTGATTGACACATAGTTATCTGACAGTAATCATCTAACATCACAATACTTATTTCTGCCTG TCACACTAATTGCAAGCAATCAATTGATTGACTATTAATGAGCATCGTGICATT/C/TJCAAGTGT TTAGGTTCTCAAGAGAAATTATGCTGTCTTCCCTGTAACCTCAAGTA
WI-5612a	44 T A ---	---	---	TGCCCTGATTGACACATAGTTATCTGACAGTAAATCAATCTAACAT/TJACACAAATATCTTATTTCTGC CTGTACACTAATTTGCAAGCATTCAATTGATTGACTATTAATGAGCATCGTGTCAATTCACAGTGT TTAGGTTCTCAAGAGAAATTATGCTGTCTTCCCTGTAACCTCAAGTA
WI-5636	26 A C CCGCAATAA	GCCAAATTTAT CCGCAATAA	CATCGAGGACT TTGGGA	TGAGAGCCAAATTTTATCCGCAATAAA/C/TJCCCAAGTCCCTCGATGGAGGCAATTCAGAATCGGG GCAGGGGAGGCAGAGGTGAGACAGATGTGAAGAAC

WI-5865c	103	C G ---	---	---	TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAAGAACTCTTTTTCATTATGCATTC ACTGACTCACTCACTTGTCTATCAAAAAATTAA[C/G]AAATATTAATATTTTATTACAGAGGAA CTCAGAAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAGGTACACAGTCCCTTCA GAGAAGACAGACAACTAAATAAATCCAGG
WI-5865b	99	T A ---	---	---	TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAAGAACTCTTTTTCATTATGCATTC ACTGACTCACTCACTTGTCTATCAAAAAATT[A/AA]CAAAATATTAATATTTTATTACAGAGGAA CTCAGAAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAGGTACACAGTCCCTTCA GAGAAGACAGACAACTAAATAAATCCAGG
WI-5865	165	T A ---	---	---	TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAAGAACTCTTTTTCATTATGCATTC ACTGACTCACTCACTTGTCTATCAAAAAATTAAACAAATATTAATATTTTATTACAGAGGAACTC AGAAGCCAGAAAAAATGACCAAGACACAGT[A/CC]AGTCTCCATCTTCAAAGGTACACAGTCCCTTC AGAGAAGACAGACAACTAAATAAATCCAGG
WI-5874	76	T G ACAGAAAA	CATAGCATGG ATAATATTAT ACAGAAAA	CCTAGTAAGTT TCAGTCAATTG ATATGT	CTCAGACATTCATTTTCATTAGTTGTTAAATTTTGTGTTATTCATAGCAATGATAATATACAGAA AAAAAATTT[G/T]ACATATCAATGACTGAACTTACTAGGTAGCAATTTGTTTGCAATTTGCT CATGGAGCCGACGTTCCAGCTCTCAGTTTTCATC[A/T]TTTTCATAATTTACTCTCTTTCTGTC ACAAATGTTCTGCTCGTTCGTTTCAACTCTCATTTGCTGATTTGGATGGTAGTCATAAAATATGGGTGATTC AGAAAAATAAGTAAATG
WI-5752	36	A T TTTTCCATC	CAGCCTCTCAG AGAGTAAAT ATGAAAAA		TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCCGATAAAAT[A/C/G] CATTAGGTATTAGATAAGCATCCCATAAAAACATTTGTTGAAACGAAAGCCGAGTTTTCGATTACACACA GTTGCTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAA CATTGTTGAAACGAAGCCACGTTTTCGATTACACAGTTAGTTGCTGTT
WI-5760b	61	C G ---	---	---	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCCGATAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAACGAAAGCCGAGTTTTCGATTACACAGTT GTCTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAA ACATTGTTGAAACGAAGCCACGTTTTCGATTACACAGTTAGTTGCTGTT
WI-5760	187	G A ---	TTCTCACCATG TTCGAACTTG	GGTGGGATCT AATTTGCA	AATATCTGGCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTTG[A/G]TGCAAGTTAGAT CCCACCTCACTATTGAGAAGCTAAAGGTAAAGACTACTCATTTCTCAGTCTTCTTCTGCTG
WI-5944	52	A G GGAATCTTG			GAGTTTAAATGAATCCTGTTCCCTCTAAACCTCTCTGTTCCCTCAACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTATGAGGAGATGCAATGTAATTTGTGATCATTTCAAGAGGTGAG TAATGCTTGGTA[C/T]TTGCTCTGTGCCGTATCTGCTCCAATCACCCATTCCTTATTTCCTATTAT GCTGAATGAAACGGTTATATTACAG
WI-5967b	148	C T ---	---	---	

WI-5967	165 C T ---			---	GAGTTAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCCCCACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTGCTGCTGTGCCGTATC/TJTGCTCCAATCACCCATTCACACTTTATTTCCCTATTAT GCTGAATGAAACGGTTATATTACAG
WI-6093	53 G C ---			---	GGGTAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGCCA[G/C]GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTCCAACTGTGCACGTAGCCCATTTGTAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTTCAGCAAACTTGAATTGACGGTGAC ACACCAATGCTTCGAGAGGGAATGAGG
WI-6141	80 T C AGGTACTT	CTTCTTAATTA AGCATCTACA		TGAAAACCCCA GAACAGTG	GACTCTGTCTCAAGAAAAAAAATTGAAAATTGAATAATTAAAGCACCTCTTAATTAAGCAT CTACAAGGTACTTAT/C]CACTGTCTGGGGTTTCAATCCCTTCACCTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAACAGGATTGTTACATGCAGAGAAATAGGGGGAGATAAAAATTTGTCITTT CTC
WI-6450	45 T G TGTACA	CCAATGACTT ATTCATATCT		TTGTTTGAAT GTGTGGTACTT CT	ATAGGACAGTTTTTCTTCCAATGACTTATTCTATATCTTGTACAT/G]AGAAAGTACCACACATTTCA AACAAAGAGCCAGGCTATGCCAGGGTGGGATTATTTACGGTCATGGTAATATGCATGTAAGACTA TTTTACTGGCCTCTTTTATGCATAAAACAAGGATTGGTCTATTCAACAACATGTGTCAATACAG CAGTTGTCATGTCCCTCTGGTACTAGAAATATAGTCTTTATAGAATATGTGTTTAGAATAAAGCCACA AATTATCTATAAAACAACA/C]JAAGGAAACGAGGCTCAAAAGTGAACAAAAACGGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAATATATCCGTGACCTCTTA
WI-6461	88 C T ---			---	GAAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTTCTGGTCACACAGGACITTTCTGGGCT ATGAAATAGTCTATTCACTGAACTAGTTATCATAAAGACATGCAAAAACCTTTTCACAGTCTTGT CCTGG[G/A]AATATCTCACAAAATTAATTAATGGCATGCGACTTTCTGATTTAGCCTGACACGG ATTGTTCCCTT
WI-7466c	141 G A TTGTCTGG	TTTTCACAGTC TTGTCTCTGG		AGTCGCATGCC AATTTATAAT	GAAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTTCTGGTCACACAGGACITTTCTGGGCT ATGAAATAGTCT/C]ATTCACTGAACTAGTTATCATAAAGACATGCAAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATTAATGGCATGCGACTTTCTGATTTAGCCTGACACGGA TTGTTCCCTT
WI-7466b	80 T C GTC	GACTTCTGGG CTATGAAATA		ACTGAA	TGCTTTTAAAAATAACAATGACCACCACCTGACACCATAGTGTCTCCATTTGCCACGTCITCCTC AGTAGAATAAGACAGGGACTTTGTCTGGTGTCTATCT/C]AJTCTCCTCAGAAAGACACTTGGCCCT CATAGGCATTCOCATAGATATTTGTTGAATGAATGTGCTTTTTCATATTGATTCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9814	104 C A ---			---	CCTCTAACCAAGAAAACTTGACTTCTCTCAACTCAAAATACCCCTCTCTAATAATTTA/G]AGTAACCA AAATATTCTTCAATAAAATTAATCTTTTAAATAGAAAGCAACAGTGTAGAGGTAGTACATTTCA CCACC
WI-9720b	55 A G ---			---	

WI-9720a	47	A G	---			CCTCTAACAAAGAAAACCTTGACTTCTCCTCAACTCAAAATACCCCTCTCT[AG]ATAATTTAAGTAACCA AAATATTCCTTCAAAATAAATTAATCTTTTAAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTTCA CCACC
WI-9825	123	A T	---			CACGCTAAGGCAGGATGTGGCTTATGAGATACTTTGCATTGCTGTGTCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGGTGT[AT]GAGGATTAG TAAGATCTCTTTCTAAGACAGAGAGAGATTATTTACAAGAAGAACTCACCAGGGTTAGTTTGCATT TAAGAAITGCCAGTCTTTTGCCTGCATCATCTTGAACATTAATCCACATG
WI-9748	74	C G	---			CCACTCAGTAAATCAATTTGTAGCAGCTTATTTCTAAAGATTTCTAAITTTTATATGTTTACCCCTTT GTCATT[C/G]TCAGACCAAGTACATGTTTTCACACAGCCATCTTTCTTTCTGGAATCTTTTCAGAAT TACAGTTATGATGCTCTTTTATATTCCCCA
WI-9943	91	T C	---			TGAGGCTATGATTGCAGATTGTAGTGACTAATACTTATTAGCAATTTCAATGTTGTGGGCACGTGT CGTTGTGTTTATATCCATCTT[C/G]ATTTTAAATTTCTACTGAGCAGAAAAAATAATGTATACATT AACCTTGTCTCCCTATTGTACCTTTAATATTGCATTTCACACCTTCCTTTTGTCAATTAGGGA
WI-9891	39	T C	---			AGGGCCCTTCACAGATCCGTGAGCTCAACACTGCCTCCCTTTC/JAGTGAGCCTGTGAACACCCCAAGAC GGCTGGTCATCAGTGTCATCCCTCTTCTTTCGGGACAACATCTTTAAAGAAAAAAGAGAGTGT CTTTGAATGTATCCATTTATCCCCAAATAATCTTGTTTAATAATCTTATTAGGCCAAATCCAAT GTGCTGAATAATCTGCCAAGCATGTCACTTACACAAAAAGGATTGTGCAA
WI-9897b	84	C T	---			CTCAGAAATATTCAGATCTCCCCAAATGTCATGATTCTTGTCTCAACATCTATTTTCCTCAAAC ATTTATCTAGCCTGT[C/G]AAGTCATCCAGTGAGGCTGTTTATCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83	A T	---			CTCAGAAATATTCAGATCTCCCCAAATGTCATGATTCTTGTCTCAACATCTATTTTCCTCAAAC ATTTATCTAGCCTGT[C/G]AAGTCATCCAGTGAGGCTGTTTATCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115	C A	---			AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGCACACCTCACCAGAACTGGAAAGGT CTGACTGTGTTCTTATGGGTGCTTGACTGGCAGGGGAGTTGAGACA[C/A]AGCCAAAGAAAAGCC TGATATTAAGAGGCACCTTGCAATTA
WI-9935a	42	C T	---			AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGCA[C/G]ACCTCACCAGAACTGGAAGG AGTGTGACTGTGTTCTTATGGGTGCTTGACTGGCAGGGGAGTTGAGACACAGCCCAAGAAAAGCC TGATATTAAGAGGCACCTTGCAATTA
WI-9983	146	C T	---			CCCTGTAGGTGCCAGAGTCCATGCTTGGCCACAATGTTAGGCTGCCTCCCCATTTCTTGTCTTGA TTCCCCAAACCCCAAGGTTCTACCCCAATCTGATCAATGCTGACTAGGTGCTGCTCAGGTAA AGCATTTATGA[C/G]TAGACACAAAGACAAAGAGGTTAAAGTTGCTGCTCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACCTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAAAGG

WI-10019	139	A T	TGATGTAATGC TATGTAGCAA ATCT	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGTTGAGTATACAGCAATCTATTTGTTTATTATGTGTCTATAAATCAATGGTTCTA ACATTCAAAATAAGATCTTTTGTCTCTCTGCTCAGATGCTTCAATGATGTAATGCTATGTAGCAAT CTAATTTCCCTAAGCACAGTAATCAAGGCCCTTCTACCCCA
WI-10020b	122	T A TTT	GCAGAGAAAG AAATCATGAC	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTAATGTTAACTGGCTCTGAAAAGAAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTTTATGGCGAGAAAAGAAATCATGACTTTTTT/AJAAAAATACC AGACTAATGATTAAATAAATAACAGTCCCTAGGGTTCCGGAAAGTGGCCTAAAGCACGTTAGTGCCT CCTTAGA
WI-10020a	39	T C A TAAAT	TGTCATCTGA CTCGTATTAA	AAATTCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTAATGTTAACTGGCTCTGAAAAGAAATTTA GGCATGCATAGAGAAATAGCAGTGTTTTTATGGCGAGAAAAGAAATCATGACTTTTTTAAAAATACC AGACTAATGATTAAATAAATAACAGTCCCTAGGGTTCCGGAAAGTGGCCTAAAGCACGTTAGTGCCT CCTTAGA
WI-10064b	170	C T TTTACATG	CCTTTAGATAT ATTGTGATTGT	ACCCTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGGCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAT ATAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGTGGTGACACTCTGTTTAAATCCAGTATCC CTACTCCTTTAGATATAATTGTGATTGTTTTACATGCTGAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10064a	54	C A CAGGGAAGG	GTAGCAGGAT	CAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGGCATGGTCAAGGGTAGCAGGATCAGGGAAGGC/AJATTATAATA AATATAATTGCAGAGCATCTCTCTCTATGCACCAGATATTGTGGTGACACTCTGTTTAAATCCAGTA TCCCTACTCCTTTAGATATAATTGTGATTGTTTTACATGCGAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10289	29	T C CAACTCTT	TCTCCTGTCCC CAAACTCTT	ATTCTTGTTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTCCCACAAACTCTTAAT/CJTAAATCCATTCAATACAAAGAAATTTATAGAA TATGCACCACATGCCACAAAGACACACCTTATATTAGT
WI-1319	40	A T ATTCTTT	TGGCACTTAG AACATAGTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATTCTTTT/AJACCATAGGGGTGTGGCTTATCT TTTACCCTGGCATGGCTTAGGTCCCTGTTTATAAATTTGGTATCTTTTGGCCACAAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTTAACATTAAACACTGGTCAGATGTTTAAACCTTGTGAACCTGCAGC
WI-10316	104	T C CTCTT	CTGTTGATTT CTACCTCTATT CTCTT	GCTTTGGGAATG TATCCAAAAGT TT	AGCAACGTTGACAACTTAGTGAGGTGTAATCAGAAGCATCTATATTATTCACAGTCAACCCCTG GACTATAGTCTGTTGATTTCTACCTCTATTCTCTTAAT/CJTAAACCTTTTGGATACATTCCTCAAGCAT CATGGTCACTTCCAGTTATGAAGGATGTTTAAAGCCCAAGC AGTGAGTTGTGCACAAATTTGGAGACATTCTGTGACCCCAACTTAAACACTTCTCCACAC/CJAC AAAGTTAACACTTCAGTTACCAGGTGATGATTGAGCAGA
WI-2572	61	C T ---	---	---	

WI-10368	31 C	T	AGGCTCTGTT	TGAAGCAACC	CAAGATAATTAT	GAGGAAGCTGCTGAAGCAACCAGGCTCTGTTCTCTACCCCTCTTAGAGAAATAAATAATATCTT
					ATTTATTCTCT	GAGATAGGGAGGAGGAGCTGAGGAGCTGGGTTTGTCTACCCAGCTGAAGCAGAAATATCC
					AAGAGGGG	TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTAATGACCCCTGATGGATTGCCTTTCAGGG
WI-10391	32 A	G	ATGACTCCCA	CTGTCTCAGGT	GGGAGTTAGGA	CTCTCCCGTTCTCTGCTCAGGTATGACTCCCAAGGTCACACTTCTTGACTCCTAACTCCCATCTCGGTG
					GTCAAGAAAGTT	TCTGCTTCCAGGGGACGCATCTGACACAGCCCTTGTCTGCTGTGACAAACAGAACATTTGCAGAAG
					GA	TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146 A	C	GCAA	GTCTTCTAATA	TGCCGCTTCCA	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAAAATATTATCTTTTTCATATT
					GTAGCT	TTCCAATTAATACTAGAAATTTCCACCAACAGAAATTTTAAACATTTTAAAGTTACCCAGAGCTTT
						CTAATAGCAAACGAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82 A	C	---		---	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAAAATATTATCTTTTTCATATT
						TTCCAATTAATACTAGAAATTTCCACCAACAGAAATTTTAAACATTTTAAAGTTACCCAGAG
WI-10567a	60 T	C	CTTT	GGTGCTCAAT	GGTGAAAATTC	CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
					TAG	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAAAATATTATCTTTTTCATATT
						ATTTCCAATTAATACTAGAAATTTCCACCAACAGAAATTTTAAACATTTTAAAGTTACCCAGAGT
						CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84 C	G	TACTTTA	CAAACCTCAA	AAATCCAACA	CGTTGGGAATTTCTATCTCACCTAAATTTATGCGTGATTAATAATACATTTTAAACAACTTCAAA
					GTCAAGGCTCT	TTGCTTTAAGTACTTTACGGAAGACCTTGACTGTTGGATTTTGAGI TTTTCTTTTATTTCTTAATA
					C	AAAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT
						TATGTATT
WI-11153a	33 C	A	AATTATG	GGGAATATTTC	GCAATTTGAAG	CGTTGGGAATTTCTATCTCACCTAAATTTATGCGTGATTAATAATACATTTTAAACAACTTTC
					TTTGTTAAAT	AAATTTGCTTTAAGTACTTTACGAAGACCTTGACTGTTGGATTTTGAGI TTTTCTTTTATTTCTTAATA
					GTAT	AAAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT
						TATGTATT
WI-2616	125 T	C	ATCC	CACAAATGTA	CCATGGCTGTA	GTTGGAACCTCCAGTATCATTTCCCTCAAAACACGCTTAAATCACAATCAGCTTTTCTTTCTGTA
					GTCCAGT	GAGCTCAAACCTCAGTCTGAATGAAATGCTGCACAAATGTAACAAGAAATGATCCTATTCJACTGGG
						ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58 C	T	TGAGA	CAAGTGAATT	TGCTCTTTCA	TGACTCAAAGGAAACACACACAAAAAGTTTCCACCAAGTGAATATGACCAAAATGAGA[C/T]AAAT
					TTTGAGGTTT	TTGTTAAAAAAACCTCAATGAAAGAGACAAATATAGTTCAAGATTCAGGTTCAATATTGT
					T	ACCTACAAAATAGGGATAGTCATGGTGTGGCAGACTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
						GAATCCATTTTGTCTTTTGGCCAGCATTTCCCTCTCCCCATATTTTAAAGGAGAGAAATTCACCTTTTCT
						CTGTTGGATGATCACAGGTTCTGCTCTCCCAATCCAGAGGCGAGGTACTATTACCCCATGGGGTTCAT
WI-10656	59 T	G	---		---	AGAGAGGATTAAACAGGGTGATGCCCTGCAATGGGAATATTGAAAAACC



WI-11169b	154	T G TTTT	TTAACCAAGA GTTTTTCATTG	CTAACTTAAAA ATCCTCAITCA AAATATAA	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATTAAGCCTAAGTAGTGTCTTTTAACCAAGAGTTTTTCATCTTTTT TTTAAAAAAGAGCAGACAT/GJTJTATCATGTGTTCTGATAAATTTTTTATATTTTGAATGAGGATT TTTAAAGTTAGCAT
WI-11169a	95	A G TTGAAAA	AATAAGTGAA AGTAACTGAC	AAACTCTTGGT TAAAAAGCAC TACIT	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATTAAGCCTA/GJAAGTAGTGTCTTTTAACCAAGAGTTTTTCATCTTT TTTTTTAAAAAAGAGCAGACATTTATCATGTGTTCTGATAAATTTTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25	A G ---		---	CAAGTGCTTGGACCTTGGATAGGTC/GJACCCGGCTGAAGTTGGACAGTTGTTGGTTAGGTTGGAG ACCAAATTCAGTCATCCTGTAAATATAGATCTGTTCCCTTTTGGGTTTACCCTAGGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTTGCTAAATAATCCAAAAATAGCCATGGGTTTGGACAAAATAC AAGGTTAGTGCTCTCTAACTTTAATGGGCATA
WI-10686	133	C T AAGG *	TGCCCTGTGC	CAATCTCTAAA TTCATGTGTAG ACACA	AATAACCTGTGGCACATAAGGCCAAATACTGAGCCCATACAGAGTGTTTTATGTTAATATTATGAAA AAAGTCAAGAGAAACAAGATGATATAGTTCGTCTAGAACTCTGAAATCTGATGCCCTGTCCAAGG/ C/JJGCTGTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAAGGG
WI-11175	77	T A A	AAATGATTCTT TCTGCTCAAAG	CTGTTCTCACA TCTTTTTTGA AA	GGTAGGATGATCTAGAATGCCACTTACAGCCACTGAAATATATTGCCCTCCCAATGATTTCTTCG CTCAAGAGT/AJTTTTTTAAGTTATCTACTATTATATTCTGCTTTTTCAAAAAAGAATGTGAGA ACAGTACAAAATGTGTTCCAGTATAGCAAAATTAATAATTAAGTAAGAAAAAGAAAGCAAAAT TGGG
WI-10694	144	A G TATGAGTTTTC	TGCAAAATGCTT TATGAGTTTTC	GGCATTTTGTA AAGGAGGAAA	TAGAGAGGCTTTTCAGTTTCAGGGTTGGAGGGTGGTGAGGTGAGATTCACCTCTTAGAAGCAGCTGGC TATGTACAGAAAGATAAACTCTGAGAAAGAACTCAGTCTAAAGTGTTCAGTCTTTGCAAAATGCTTTA TGAGTTTTTC/GJTTTCTCTCTTTACAAAAATGCCATCAATCTCTCAAGGAAAAAAGAAAGCTTTCT T
WI-2716	23	T C C	TGAATTCATCC AGAAAAACAG	TCTCTTTTCTC TCTTGTTGTCA TTC	GTGAATTCATCCAGAAAAACAGT/CJGAATGACAACAAGAGAGAAAAAGAGATAAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCCAGTGCATGGAGCAGTG
WI-10719	115	T C C	TGACTCTCAAG GCCATTCTAG	GOACTGCCAGC AGCC	CAGGCCCAACTCTGTCTAATTAAGTGTTTTAGAACAGACACCTCAGTCACACAAAAGTTCTCTTTGTATGT GCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCIAGT/CJGGCTGCTGGCAGTGCTT TCCAGCCTGCTGCCCATAACTAA
WI-10721	40	A G CTGGCCA	TGGCTCTGCTA	GAAACTCCAC ATAAAATAAT CTCA	CAACCAATTCAGATTTAATTTTGGCTCTGCTACTTGCCCA/GJATGAGATTTATTTATGTGGGAGTT TCTGAAGATTCCCATGGTAAATAGTATTCCTCTTCCCTGCTTAGGTTTTGAAGAAGTTGAA

WI-11204b	88 T C ---	---	---	GCACACGAAATTGATTAAATTTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTTACCTTTT/CJATTTTAAAGTAACATAAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAAAATTTATTCAGAAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAGGG TGAAAAGAAA	TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATTGATTAAATTTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTTT/AJACCTTTTATTTAAAGTAACATAAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAAAATTTATTCAGAAAG GCAACATC
WI-10732	80 C A ATTGGTTCACT	GCTGTGCTTC	AAGAACAATG CATAACAGAA CTTTAA	ACATGTAATTTCTTTAGTGGTCAGCCTTCCCTACCCCAAGAAATATCCCTGGTTTATTTGCTGTGCTTC ATTGGTTCACCT/CJATTTAAAGTCTGTATGCAATTTCTTTGAGTCCACATAGGTGTTAATCATTCCA CACCACCTCTGTTTAACTGTC
WI-11206	127 A T ACTC	GGTTGTGTTTT CTGTATGTACA	GAGTGACAATC CTAATGGTTGG	TAGTCTTTCTTTGTACGAGTGTCTATAAAGAAATTACCACCTCTGTCACATTTTGTAAAGATAGCACAG AGAGAAAGCATTACAGGGCACAGCACAAACATGAGGTTGTGTTTCTGTATGTACAACTCJATTTCCAA CCATTAGGATTGTCACCTCTCATATATAGACAGAAATTCAGTGGTGGTGAATTTGAATTCACACATGGA ATAAGTCTA
WI-11215	68 C T ---	---	---	GAAAAAAAGTTTAAATTTGGATTGCTAGTTTGTCTTAAATTTGACCTACTTTTCAGATTTATTTTAGT [C/T]ATTTTCTCTATAATTTCTTTGTAAGTATGGATTTCTATAAATTAAGGAAACAGATATTT ACACAGAGAAAGACAGGATTGCTTGAATTAGTATACATTTCTTTATCCAAAGCCCCATTTCCACCATGT TTT
WI-11219b	89 G A AGAGAAA	GAGAGAATAT TCCAAAAAGT	GGTCCCTCTAAT TTTTCTACACT TTCT	ATGAAAAATGCATTAGAAGNATTGGAGGATAAAATTTGAGAGAATATTTCCAAAAAGTAGAGAAAAA GAGACAAAGAGATGAAAAATAGGA[G/A]JGAAAAGTGTAGAAAAATTAAGAGGCCATTTCTATACAG TCCAAATATTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11219a	18 G A ---	---	---	ATGAAAAATGCATTAGAA[G/A]AATTTGGAGGATAAAATTTGAGAGAATATTTCCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAAGAGGCCATTTCTATACAG TCCAAATATTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11222b	136 G A GGCTGG	CATACCACTGC AGTTGTGA	CCTGGTAGCCA AGTTGTGA	AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAATGCTAAAAATTTGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCCGTTGAACATTTGTTAAACATTTACCAGCATACCAGTGGGCTG G[G/A]TCACAACCTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTTGCTTTTCACAGGCTACTGG AAAGCC

WI-1122a	25 C T A	GCACAGTGG AATCATTAC	TTTTAGCATTT GCTGATTTCG	AGCCACAGTGGGAATCATTTACACTA[C/T]CGAAATCAGCAATGCTAAATTTGGGGCTTTGGATTTT TGTTTTGTTTTTCCATAGACOCACCGTTGAACATAITGTTAAACATTTACCAGATACCACCTGCGG CTGGGTCAACAACITGGCTACCAGGAGAACCTGACACAGACTTCGTAATGCTTTACAGGCTACTGGA AAGCC
WI-10775	39 C T CACTC	TTATGCCATA TTAATTCATTA	CTAGATGTAAT TGCTAAGAAA ATATGATG	TTGCAAGTTGTTTTATGCCATAITTAATTCATTACACTC[C/T]JACATCATATTTTCTTAGCAAAATACA TCTAGACACCTGGCACTCAGTAAGGATAITCTTGGCAGGATAATCATTTGTTATCATTTAGACATTGCA GGAACCACCATATGGATGATAAATGTTGTTTAAATGAAGCAAGCAATTA TTGCATGCATTTATACGAAAGGAATTAATAATATCTTCTTATAGTTGAATTTTAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATAGAAAAATGTCAAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA[A/C]GACATAGTTGCTAAGGATAITCCACAAATTA TTCATGA
WI-11226	165 A C ---	GCAGGGAGG AACATTTACA	---	CAGTGGCTGGCTACTGACAAAACGTAACTCGTGGCAGGTGGCAAGGGAGGAACATTTACAG[A/G] TCCATCTCTGATGTCACAGCAGGGCCAGGAAGGTTGATCTGGAG TGGACACACTGCTCTAGACC[C/T]TCCCAGGGTCCCTCAAAGGTGGGTGTAGAGGCCCTACTGCCCT GCCCTGGGACCGAGAGGCATCAGGGCCCTTAGTCTCTCTGGGACAGTGAAGGGCCACCCACC ACAGAAAAATGCCTAGGCTTGTAGCAAGAGAGGAAGCATCTTCATGGGCAGGAATTC/TJCATTT CTGTGTTCTTAGGGTTGTGGCTGGCCATCAGTTCAACTCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACTACCCCTCTAGAAGTCAATGCAAAAGAGAAATGATGA GGACCAACAGAAITTAATCTTGGCA[T/C]JAGGGTTTCTTAAACATAITTTCTGCAGAACATTTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACITCTAAAAGGCTATAATATTTGGATACATAGGCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10828	23 T C ---	CATCTTCATGG GCAGGAATT	---	TATGCCCTTCCCAACGAGCCATCCACGCTGCTCTTAGCACAAAAAATAGAAATACATCTCTGAATG GGCACAATTAATCTGCAGGCTCTCC[G/C]TTTCTAAGTCACCTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGAGGAGATGAGAGAGGGCTGCTCCGTGAAATAC TAGTTCGG
WI-10832	91 G C AGGCTCTCC	CATTAATCTGC AGGCTCTCC	GTGACTTAGAA A	GATTGAGTATTATCAAAATTTGCCAAAGACCATTAACAAGATTTAATAGTTAAAGCCAAAACATATA AAGAAATTAACGTGTTCAAAAGTGTGTTAA[T/C]TCTAATACCAATTTTATAGGGCCACCAATTAACCT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT GGATGATGTTCTGTGGTCCCTTAT[T/C]JAAAGCCTCTTGCAATCCCAATGTGTAAATATTTTATCT TGGTATTTCTCGCTTACCATAGTCACTGTCAAGTGTTCCACCCCT
WI-10834	96 C T GTGTTAAT	AG	AG	
WI-2287	24 T C ---	---	---	

WI-2296	81 A	G	TGTTACTTTGA TTCTTTGCTCT	GCAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGGCTCAGGCTTGAATAGAGTTGTTACTTTGA TTCTTTGCTCTGAC[A/G]CCAGTTAGCTGTGTGATTGAGAAAGTTACATTTGTTGTTG
WI-2300	77 G	T	GGCACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTTCCCTGGAAATTTCCCTTTATTTAGCGGGGCGAGGTGGTAGGCACAGAACG CAGTCATAC[G/T]TGCTTTAAATGACCCCAACCATTAAGTAAGATAGCATTCA
WI-2371	55 G	T	GTCTTGTTCTT CCCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGAAAGGTGGTCTGGTCTTCCAGCTTCT[G/T]GTGGTGGCT GTCAATCTTTGACATTCCTGTCTTGACGTGTATAATCCAAATCCCTGGCTCCAGCTTTACATGATGT TCTCTCCGTGTGTCTGTG
WI-2395	122 A	C	GAACATATTT GTAGAAAAAT TACTATCCAA	TCACCTTTCTA TTTATTCTGAA TTCA	GGGGGCACAAATTTAGCTACAGTGCATATTAAAAGATAACATAGAAATATCATATAACTTGGTTTAC TGAAATCTGAAAGCTTAGGATGAGTGAACATATTTGTAGAAAAATTAATCTATCCAA[A/C]CTGAATTC AGAATAATAGAAAGGTGAATCATCTTATCATTAAGAAAGCTAAATTAATAGTAACAATCTTTA CATTTACACAAACCCA
WI-2437c	192 G	A	---	---	CACCAGCCACCACCTACACCTCCTGTGGGAGTCTGGCTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTCTGCAAGAGGCAATCGACGAACATCACAGTG[A/G]GCTGTG GTGCCAAGGACGCAATTATG
WI-2437b	179 G	A	---	---	CACCAGCCACCACCTACACCTCCTGTGGGAGTCTGGCTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTCTGCAAGAGGCAATCGACGAACATCACAGTG[A/G]GCTGTG GTGCCAAGGACGCAATTATG
WI-2437a	128 G	A	---	---	CACCAGCCACCACCTACACCTCCTGTGGGAGTCTGGCTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATG[A/CTC] TAAATAGATGGACTCAACCCCTTCTCCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCAATTATG
WI-2440	71 G	A	GCAACCTACT GACAATTTAA TTTTAGTT	AACAACCTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTCTCTCCTTAGACCCCTCCAGAAAAATGCAACCTACTGACAAATTTAATTTTA GTTG[A/G]GTGAGACCAATAGCAGAGTTGTTACCTGCGAAGACT
WI-1356	123 T	C	TGTTTAGGAA ATAATGACAA GAAAAA	TGTTTACAACCT GTACCAACAT G	CTGTAACCTACACATCCTCCTGTAACCTCTAGGTTACTTGTAAATACAAAAACACAATGTAAATGCT ACATAAATAATTTGTCATATACTATTGTTTAGGAAATAATGACAAGAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCAAGCAATTTTCCCCCAATATTTTCAATCCACAGTTGGTTTATCCACAG AAACCACGAATG
WI-2886	46 C	A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGAAAG[A/C]AACGAGATAAAGCATG GCAAGACCACGCTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTCAGAAAGAAACAGAGGAGCGTT

WI-2906b	77	T A	---	---	CCTGAACACCTGGAGCACTTCCCTCCCTTGACACCTTCATCTTGTGGAACTTTGCCTGGAATGCTCTTCCCTCTT/AJGAGCTTTGCTGGCTTACCTTTCTTTTCCCTTAGGTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTGCTGACCAACAA
WI-2906a	50	A C	GACACCTTCATCTCTGCTGG	AGAGCAATCCA GGCAAACT	CCTGAACACCTGGAGCACTTCCCTCCCTTGACACCTTCATCTTGTGG[AJ]GACCTTTGCTGGAATGCTCTTCCCTCTGAGCTTTGCTGGCTTACTTTTCTTTTCCCTTAGGTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTGCTGACCAACAA
WI-1736	175	C T	---	---	TACTCCTCATTCCCTCATGTCCTAGACGTACTCAGATTCCATGCCCTGAAACATTTATTTCCCTAAATAGATTTCGACCCCGACACTATTTACACAGAAACAGCATGGAGCAGTTTGGAGCTGGCTCTTAGAGAACTTAAAGGACAGTGGTTTCCATCTGCTTCCCA[C]TJAGAGATCTAGGGTGCTTTTGGAAACCACCTGG
WI-1851	136	G A	GTGTTAAGTA	CACTAGCAATG TTAAACTGAAG TTG	AATACCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTAAACATATTATCTGGGGAGGACACAAACATTTAGACCATAGCATTTGAATTAACATATAGATGTGTTAAGTAATTATTAACATGGTACA[G/A]ACAACCTTCAGTTTAAACATTGCTAGTGATCCATGTGGATACCATGTACCTTCTTACATCATGTGA
WI-3000	62	G A	AGAGACCCC	GCACATAGG ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTACACCCAAACACAGAGACCCC[G/A]TGAGCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGATAGTAGACACT
WI-1754	177	G A	TAGTC	TTTCTCCCTT CTTAAAGAGA	ATGATCTGCTCAATTATAGTCCCAGATAAACAGCCCTTCTCCCGCCCAACCCCGGATTATTTTACTTAAGGGTTTAGCAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCCTCATAAAGTGATTTTCTCTTTCTGTTTTGTTTTCTCCCTTCTTAAAGAGATAGTC[G/A]CCAGAGGCAATTCGACTTTCTGTAGCCACAAGATT
WI-3167	37	T A	TAGATTC	AAATCAACG ACAGATCTAT	ACAACACAGCAAAATCAACCACAGATCTATTAGATTCTT/AJACCCCATCTCAAAACTATCACATCAAGAAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140	G A	AGATAAAGA	TCACTCAAACT AGGCTTGG	CAAGCACACATTCAGGCAGTGGCAGGTAGGGAAGGTGGCAACTTGGCGACGACAGAGAGGAGGAAGAAGTTCAGACCCGTTGGTAGGATAAGTGGATCCAAACCCCTTGTAGGGCAGGTGGTGAGTGGGCGAGATAAAGA[G/A]CCAAGCCCTAGTTTGAGTGACACTGTGGGGATTCAAG
WI-1775	47	C T	TTTCTCTG	AGTTGAGATT ATGACAAATGAT GTAAA	ACTCCACCAACAGTTTGTGAGCCAAACCCTGCATGGTCTTTCTCTGCTTTTACATCATTTGTCATAAATCTCAACTGACACATCAGTGCTCTGCCACCCCA
WI-3402	55	G A	ACAT	GAGGACTTAAA AAGGAGCAATT G	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTGATTTCCTTACAT[G/A]CAAATGCTCTTTTAAAGTCCCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCCTTAGGAC

WI-3416	33 C T	CCAAGTTGTA GCAATCAGAA	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCCTCCAAAGTTGTAGCATTTCAGAAAGTCCTCTCTTAGAGGTAGTTGCTCGTCTGTTAAAA TATGTTTCAAGATAGTATCTCCCTGTTGTCACCTCTCCCAACAAGTGTACCAACAGCAATGTTTAAG GAAATGTCAATGCTTGTACCTCTGACGCACACATAATTAATCCCATTCCTTAAAAAGACCAGG TCCTATTCTTACAACAACAGAAATTTAACAATTTGAAATTCAGTACTCTCTTAGGCCCATCAGAG AATTCATGATGAGGAAATTTGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGAGAG AATTACAGTTTACCAGGACACAATCCCACTTCCAGAGCCATCTGTAAAGAC CATGCTAGGTAGTCTGATCATGAAGTTTGAACAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCACAGTATTTAATGAGGTGGTGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3453	70 C T	TTCTAGGCC ATCAGAGAA	TCAATTTCCC CATGACTTC	TCCTATTCTTACAACAACAGAAATTTAACAATTTGAAATTCAGTACTCTCTTAGGCCCATCAGAG AATTCATGATGAGGAAATTTGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGAGAG AATTACAGTTTACCAGGACACAATCCCACTTCCAGAGCCATCTGTAAAGAC CATGCTAGGTAGTCTGATCATGAAGTTTGAACAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCACAGTATTTAATGAGGTGGTGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474b	109 G A	---	---	CATGCTAGGTAGTCTGATCATGAAGTTTGAACAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCACAGTATTTAATGAGGTGGTGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90 A G	AGTCAGTTTCC CTAATTTTAGC AC	CAACCATCAAT TTTCTCCCA	TTTGACCCCATACATGAGATAAAACCATAAGAAATGGTGGAAAAATAAAACGGGAGAGACCTGGG TTTCTGGATGTCCTCTTGGAGACAGGGTCACCCAC TCACGGCAAGTTCTGCAGCAGTCTCTGACTCCTGCTGCTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGGATA TAAACATCTGCTGAGAGGCTGCACCTGGATGAGGTCACAAA TCACGGCAAGTTCTGCAGCAGTCTCTGACTCCTGCTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTCACAAA
WI-3600b	146 G C	CCATGCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TAAATCATGCTTATTTTACAAGGTATCCACTCACATAGGCAATTTGATGTGATCTCTTTCTGTAA GAAAGCTCTCATGCTCTTCTGAACTTCTACTTACTGTGCTGTTATGATGCACCTGGTCTTTTGG ATAGATGGTTGATAGGAGATGGGTTGTTAAGACACAAATTTACCTTGTGTTTCAGGGCAGAAATAG ACTCTCTGTGTATCACTGAATGAGTTCCAAAAGCCTTTATGCTTAC AAAGCGATGTTGAGATACCACATCCATGAAAAAGTAAAAACACACACACAAAAATGACATAAAA TTC/AAAAAATCTATAGTTTATGAAATGACTTCCAAAATTCAGAGAAAAAGTCACTTAAACAGG ATTCTCAATTCATCCAGAATACTCCTCTGTCTTAACTTTGACTGCACAG
WI-3687	67 A C	---	---	TCTAAATGTGAAACCAAGAAATCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAACTTCACACCGGTTCAATGAAAAACAATGATTGGTGAGCCATGTCCCTTATTTAATGAAAA GATCTGGGCAATTAATCT
WI-3735	72 T C	CCTCAGTTATG TATCAAAATGA AAAC	GGCTCACCAT CATGTTTTT	

WI-1819	51	C T	---			GAAAAAGCAGGAAGCCAGGAGGACAAACCTTTTGAAAAAGCTTTTCAGCAC[C/T]TCGTGGATCCG AATTTAGTGTGATTTGGCAGCAATGCGGGTAACATGTTCCAGTGTTTTAACTTCACACAGAATTGC CAGATTAGCGATTGTTGACTTGCCAAATTAATGAATGTGGAAAAAAGGGTGGTAAGTGT AAGCCTGCTGCAATGTTAGACACGAGGTGGGGTGGGAGGTGAATACC
WI-3746	116	G A	---			GGCCTATTACATGACACTGGGCCAAGATCTTGCTTCCCTTTCTTCAATAGATAGACTAAGTAA ACTGCCCTGGCCAGGAAGATGTTGTCTTCATCATCTCTGCTCTG[C/A]GCCCCAGGATAAAGCA GGCA
WI-3867	49	T C	CAA	ACAGTCATTT AGTCTTCTGA	TAAGATAACC ATACTAGGTAC	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTGACAA[T/C]CGGATGTACCTAGT ATGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAAGACACAGT CATTAAAGTGAGAGCCAGCATCTAATCAGGCTCAGTGAICTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25	A C	G	TGACCAATGTC TTTAGAAGCA	TCGTGGGTGTC CTCTCC	CAATGACCAATGTCTTTAGAAGCAG[A/C]GGAGAGGACACCCGACGAGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGACGCCACAAAGGTGAGGAAGCAAGGTTGCTGGCCACT
WI-3901	114	A G	---			GGACCATTTGCCCTCAGAAAGTACATTCAAGCCCTGGACGGTGTCTCTCAACACTGTGACCTCAGGCA AGTCATGCTGCTTCTTCCCTGAACCTCGGCTTCCCTCACCTGACAAGTGG[A/G]TATCATGTGCTACACTGC AGTGTATTAATGCTGCAT
WI-3914	99	C T	GC	TGATCTTCTC AAGACTCACA	TCTAGAAGCAA TGAAGGATGG	CTGAGGAGATTGATGCTACTTTACCTGAGGAACTTTTATACCTCCCTGAGTTTGTGCTTGCCTTGC GACATTGCTGATCTTCTCAAGACTCACAGC[C/T]ACCATCTTCACTTCTTCTAGACCTATAACTAG ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAAGGTACAAAGTGTGACCCATGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G A	A	CCAAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG	CCACTCCCAGGCCAAGAGCGTCTATGAATCAT[G/A]CATTTGTTCTCTGTTATTGCTGTTACACAGAGT GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC
WI-4091	84	A T	GTCATTGCATG	TTGAGGTCCTTA GCAACAATAT	TGAGTTCCTAT TAAGTGACAAT ATTGTT	TAATTCACATTGCTCTGTTTGTCATTTATTGCTTCTCTTATGTAACACAAATCACCAACATTGAGG TCTTAGTCATTGCAIG[A/T]GTATAACAATAATTGTCACCTTAATAGGAACCTCAAGCATAGTTATGTGT ACATTTATTGCTAACAGCAG
WI-4160	117	A G	CAACAGAA	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC	TCCTCTCTGTAAATAGGAAGTCTGATTAGATGCCCTTTTGAGGTAGGTTGGCTTCTAAGATGGTAATT ATCTGTCCAAGTTTGTGTTTCTCTAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGCATCCCTCGGATCTGAACGTTCTTCATGATACT
WI-4168	32	A G	AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA	CGTTGCTGGTGAGAGTCAAAATTGATACAAACA[A/G]CTGAAAAATCTGTTGGCAATCTATTAAGG CAAATATATACCAGCAGTGTGGTCTAGCAATTTCACTGCTGGGCATTACCTAACATATAATGAT

WI-4177	68 T C	TGAATAAGCA CGTATTAAAT TACCTA	AAGGCAGCAA ATCATGATG	ATGCCTGGGATATACCTTCACAAATGACTAGTAGTAATAGCACGTATTTAAATTTACCTATTATATTT AT/CJCATCATGATTTGCTGCCCTCTTCACAAATTTACTACAAAATTTGTTATGTCACATGAGGCACATG ATCCCAITTAACCCAANTAG
WI-4199	51 A C AAAA	CTCCCCAAGTT AGTCAATATA	ATATGTTGATT AGGTATAACA ATATGTTG	GCCATGAGCAGAGGGTGAAACCACCTCCCCAAGTTAGTCAATATAAAAAAA[A/C]CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAACAA
WI-5163	24 C T CTGCTGT	CTGTCACTGGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACCTGGTCTGCCCTG[C/T]GGTCTGTTCTCTGTTCCCTTTCAATGTTCAACTGCTTGAT CTGTGCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGGCTTTGTAGACCAGAGTTTTCTT GGAATTGCAACATTTGGGCAT
WI-4250b	117 A G ---	TCAATATGAG TCTTGTGAAAC	---	TAAGTGCAATTAACGTACAAAGTCCACAAATACCTCTTCCACCAGTGCTAAAGCAGTTTTTAATAACA GGTTCAATATGAGICTTGTGAAACAGGGGTGGGAAGGATCCTGTAAAAGG[A/G]TAAATATTGTTTT CCATAATTTGAAGATGTG
WI-4250a	94 G T AGG -	TCTTGTGAAAC	CTTTTACAGGA TCTTCCCAC	TAAGTGCAATTAACGTACAAAGTCCACAAATACCTCTTCCACCAGTGCTAAAGCAGTTTTTAATAACA GGTTCAATATGAGCTTGTGAAACAGG[G/T]GTGGGAAGGATCCTGTAAAAGGATAAATATTGTTTT CCATAATTTGAAGATGTG
WI-4255	68 G C CACCT	TGCTCCCCCAT	GGCCTACTTCA AGTTGTGTAAG G	TAAATGTCCTGGGGAGATAATAGGAAAGGTCCCATCCCTCTGTATACCTTGGTTGCTCCCCCATCACCT [G/C]CCTTACACAACTTGAAGTAGGCCCATCCAAACACTGGTGAGAAGAGTAATACIGTCGAC
WI-4256	57 C T ---	---	---	ACAGCCTCTTCAATGGCACAATCAAAAGCACCCAGTAAAGCAGAGGCAAAAATCTGG[C/T]CTCAC CATTGGAAGATCTTCTGAAGGATAAGGAGTGAATGACTGCTAGAAGAGAAATGATTGGCCT AGTTCACTGCCTAGATGAGTAGACCATGTGCTTTGTTAAATGTACATGGGAGAGACOGGAAATGG GATG[C/T]TACTATAGATAATCTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4325b	71 C T ---	---	---	AGTTCACTGCCTAGATGAGTAGACCATGTTGCTTTGTTAAATGTACATGGGAGGAC[C/T]GGAAA TGGGATGCTACTATAGATAATCTTTTAAATGACTCTTCTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58 C T ---	---	---	TGGCAGAAAGTCGGGTATGGCAAGTCAGGTGGGTAACTTGGATGCCACTTCTGCCTGTCACCTTCT CTAGACTCTTGACCCCTGCAGGAGGATCCCTGGCCTCCTGAGTTTATCATCTCCACCTCCAGCCACG GGCCCTGTATCTGTTTCAGGCC[C/A/G]GATCGTCACGGCTCACAACCTGTGGGAGGTAGGAATGACGA G
WI-4347	158 A G ---	---	---	CCAGTCTAGGCTGCAAGGACTTCAATTTCTGGGCAAGTCTGGTGTGTGCTAGGGTCAGAGGCGGAGCG ACCTGAGGGACACACAAACAGTGGGACACCAAGGGGTACTTGTATCACCT[C/T]CTCCCGCAACCCCA AGCAGCACAGCTTGACGCTCCAGGAAAGACTCCTTACTTCCACTTGAGAAAAGGAGAGGGGAAGAGA AAAGAGGACTTTGACACACAACCTTGA
WI-1936	117 T C ---	---	---	



WI-5204	54	C T ---		---	TAGATTTGATTGATGACAATAGGGAAGCCTTTGTTAAATTTGGGTTTTGAAGAA[C/T]GAAGAAAA TGGAAAGGGAAGATTGACAGAAACCAAGAGAGTGTGAGGGGCAGCAATCCAGTTTACTGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70	A G C T C A A A A A	GGACCTTAAT ATTTAACAGA	AGATAATTTTG TAAAGATAGTT TTGGC	TTTCCCTTATTTATTAGGAAGCAAAATGTTTCATACAGGACCTTAATAATTTAACAGACTCAAAAA TAT[A/G]GCGAAACTATCTTTACAAAATTAATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112	T G A T A A A	TTGTATCAAA GAGATGGGGT	AATTAAGAA ATCTTTACATG GTTCTTT	CCCTGAATGTGCTTTGCTTCTCCTCCAACTCTCTAGGGAACTTTTCCATGTCAGGTGAAGTTTTGA AGAGTACTTTTAATTAAGTGTATCAAGAGATGGGTATATAAT[G]AAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTTTCATCAGGGCTCTTCCACTGCTATCAGTAAA
WI-4456	49	C T T A G T T C C	AGTTGAATTA TTCAGAAAAAT	TTTCCCTGTTAT GCATGAACCTTG	ACACATTTTCATTTTGCCTTAAGTTGAATTTATTCAGAAAAATTAAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACCAGGTTGGGCAATTGATTGAATTGT
WI-4461	49	A G C C T T C C	TCACTGTTATT TTAAAATTAT	TTTGACCTTTC ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAAAATTCCTTCC[A/G]TGAAAAATTGGTGAAA GGTCAAGAAATGAATTCACATTTTAGATTCTGGAAATTTTATTTGCGATGATAATGCAATGGGC
WI-4465b	75	G A ---		---	CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGTATATAAGAAAAACAGTTAGTAATCTT TCACCTTT[G/A]TATTTCTCTCTACCTCAGGGAATC
WI-4465a	41	A G A C A G A A G T	AAGCCAGACA ACACGAAAGT	GGTGAAAGATT ACTAACTGTTT TCCTT	CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGT[A/G]TATAAGAAAAACAGTTAGTAAT CTTTCACCTTTGATTTTCTCTCTACCTCAGGGAATC
WI-1949b	160	T C T A A T C	GAGTGAATAA ATGAATGCCA	TGAGAGGTGGG GACAAAAA	GGGGTAGGACCTCGAGATCTTTTCAGAAAGCACAATTCAAACCAATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G]CAAGGCTGCTGACATGGCTGAATATATGTTGAAGAAATAAA GGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-1949a	86	T G A T G C T C T G A G T	CAGTGGTGAG ATGCTCTGAGT	CCATGTCAGCA GCTTGG	GGGGTAGGACCTCGAGATCTTTTCAGAAAGCACAATTCAAACCAATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G]CAAGGCTGCTGACATGGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-4529	64	T C A A G A T G	OCAAGTAAGT CTATCATTTCTG	TTCTAAAAATA ACACTTCCTGA AAAA	TGAGAGAGTTTTGGATTATTCATCCTCTGCAACACTCCAAGTAAGTCTATCATCTCTGAAGATG[T/C] GAGTTCTCTTTATATCCTATGATTATTTTTCAGGAAGTGTTATTTTGAATATAAACTCCTGGGT CCATCCAGGCTAGGGTCAATGGCATCCATCCATGGGTCCTGGACAAAGATGGCCCTTAGGATCATTTT

WI-4540	110	A	G	GCACATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTCCCTTTCTTAAAAATTGGTGCCATAGTACTGGCTTCTGTGTGTCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCC[A/G]JGTCATGGCTGCTATTTGCCAGTC AAATGAGACAACCTTCCCTAT
WI-4582	226	T	C	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACGAGAACATTAAATTCACCAACACCCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGGCCAGTTAACTTATTCTCTGTACACA AATAACTTTATGGGAGACAGCATTTGTAATCAATCAATAAATGACTCGGTTGGCTGTACAAAGCAT AAACAGAACGCTTGCAAAATATGGT[C/C]CCTCTGCTAGAAACCAATTTGAT
WI-1965	105	G	C	AG	GAATGGATGGG TCATCTCTCT	CAAAGTTAGTTAACTTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCAATTGAGGAAGTGTAAAG[C/C]JAGAGAGATGACCCATCCATTCCCTGG GCTTCTTATATGACACCATACTATCCACACAGATGTGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
WI-5248b	99	C	T	TTG	AGAAAAGAG AAGAAGGGAA AAA	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTTAGAGCAACCCAGAAAATTTAAACGCCTAC CATTTTCACTGTTTCTATTGACCGTACTT[C/T]JCTTTGCTTTTTTTTCCCTTCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-5248a	38	G	C	CTACGTTGT	TTTTAAATTTTC TGGGGTTGCT	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTTAGAGCAACCCAGAAAATTTAAACGCCTAC TACCATTTTCACTGTTTCTATTGACCGTACTTGTCTTTTCTTTTCCCTTCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-4596	69	T	A	AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTTGACTTTGCTCTGAAGCAGAAAAGCACTGTGA C[T/A]CATTTAGGCCCATCTCCTGCCGAGCCCTGCCACAGCAATTTGTAAACATATGGCATTGGG ACATACTCTGAGCCCCCACTATTGACAAGATTCTCCTTTTTTAAACAA
WI-5252	119	A	C	---	---	GAAATAGGGCAAAAATTAAGACTTCAATAATTAAGAAAGTCTTGGGAAAAGGATTTGTGATGATCATTG AATCTGTTTAAATACAGAAATTAATACTGAATACCTGTGTGAATCATTTGCTTT[A/C]JACCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61	A	G	CT	TTAGGTGCTTA AGTTGCTACT TGG	TGCAAAAAGGAAAATGATAACCAGGACGTGTTGTTCAAGCAATGCTAGAAAATTTATGCCTA[A/G]C CAAGTAGACAACCTTAAGCACCTAAGGCAGAAATGAAGTTTCTCTCTGTGCTAATGAAGTCTCTATTCA ATTACCAATTTATCGGGTAAATTAACACTGGAAAGTAATGCCAGGCTAATTTGTTAGATTATGATAAT TACACGCTTTGCTATGCT
WI-5257	77	C	A	GCAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATGCGGGGCAAAATTAAGCATATGAAAATACCAAGTGTGGCAGAGGCATG AAGCAAGAGG[C/A]JCTTTTCATCTGCCCTGGTGGTTTTCAGTAACCTGCAACATGCTTTTGCCTCC CGGATGAAAAGATACCCCTTCTATGACTCAGCAATTCACCTAGGTATGCACCTAACACATGGGTG GCAAAAT
WI-4649	50	C	T	TTCCGAATG	TGTACTAGGTG TACTTACAAGA AATCATC	TCAGTGTTTAGAAAATTTCTTCTCCTCAGTGAGACCATTCTTTCCGAATG[C/T]GATGATTTCTTGTGA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGCTACCTGAATTTGTATTTTTTAA AAAATCCTCCCAATATTG

WI-4650	148	A	G	G	GCACAAAGAA AGTATAAGTT GTCCTT	CTGAAGTGTTA AACTGGATTG G	AACTGTGGTATGTAATGTTGTTGTTGTTTCTGGAGAGTCAGTACTCTCACTAGATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCCTAGAGCACAAGAAAGTATAAGTTGTCCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTTAAACATTCAGTAACGTT
WI-4677	82	T	C	AAA	TCCAAAAGTG ATTAGGTGAA CTT	TTTCAACAGTG TCATTATTCAA CTT	AATTGAGATTTTGAACATACGTCGACATTTTGGAAAAAATTTGCCAAAAAGTGATTAGGTGAAAAAAT GAGTTGAAATAAATGTT[C]AAGTTGAATAATGACACTGTTGAAAAATGATGAATCTGCTTTCAATTCA CATGAAAGGAGACTAGAACACAGCAGGTTTATAGGGGAATACAT
WI-4698	135	C	G	---	---	---	ATGATGCTATCATGAGGAATCTGTAGAAAAATTTACCTGGCAATGATTCAAATAAAGTTTGTC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTCTTTGACGGGAAAGAAACTTCAA C/GTTTCGAGAAGGCTTAGATTATATCGCTGAAGCCCCATTCTG
WI-4722	88	G	A	AACACCACAG	TGCACATATGG G	AATATGGAATC TGCATTGAGTT G	CTTCCATTCTGCCAGTTAGATGACTGCCTCTCCACCAGCCTAGAAAAAGATGGGAGATTTATTTTC TGCACTATGGAACACCACAC[G/A]CAACTGAATGCAGATTCCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	---	GCCACAGTAAAGAGGAAAAATGGAGCCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTAAATCATTGATGTTGAGATTTTCAGAAAAACGTGAAATTTATTGAGTAACCATGGG TCAACTATGAT[C/A]CCAAAACAGCAGTGTGCTAAAAAATATGATAGTTTCTCTCTGTCACCC GCAATGAAAAGGAGTT
WI-2028	176	T	C	CCTGTCTCATC	TGTTTACGTTT G	GGTTGGAACT CAAATTACCTA GAA	GACTACAGCGCACAGACAGGCAATGTGTGGCTTGACACAGGTGTTGGTTTGTGTTTAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGGCTCTTCAGTTTACTACAGACCTCATCATCTCCTGGTCTCTTG CACCCAGTCCACTTCACTGTTTACGTTCCCTGCTCATCT[C/J]TCTAGGTAATTTGAGTTTCCAACC TGTTGG
WI-2033	183	T	C	A	GGGTGCTAGA ACTAATCCCTC	CAGTGGTTCCA CGTTCTCC	ATGTGTATGAGCTCCACATTCGCAGATTCAACCAACTATGGATAGAAAAATATAGTATTCCTCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAATTTTCCAAAGTTTATACAGGACCCAGTGTGGAAATTT AGCAATTCCTGGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA[T/C]GGAGAACGTGGAAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	---	TTATGGATACATGTTTCTGGTGAAGGACAAGAGTTGAAGCAAAAAGGACAAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCCAAGGCTCCTTCCACCAATCTCCACTTCTACTCTGA[T/C] AGGCAGACTTATATGAAAAAAGGGA
WI-2034	150	T	C	CCAAGGAC	CCACAGTGCA CCAAGGAC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGCTTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGCCCAAGA CCTCCTTCTGCGGTTTTCAGTGAAGAACGATGAACCTCTTCTATCTTACAGCAGCTGGACTTCACCA CAGTGCACCAAGGACT[C]GGACCTGCACCTCTATCTTTACCCCTTCCGACACCAAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155 C	T	TGTCCTTTAAA GTGTGTAAGT ATTAATTAG	ATTCTCTTCTG AAAGAAACAT CA	TCAGGTGACAAGAAAAAGTCACATTTCTTCAATCACTACCCATTGCTGTGTTATTGCTCTTGCAGTGT ATCCAAGGATGTCACATTTTGGAACTCTGTAGATCAGAAAAAAGTGTGCTTTAAAGTGTGTAAGTATTAA ATTAGATTTCTATTTTGATA/C/TTTGATGTTCTTTCAAGAGGAAAAATTTGTGTAAGAGGATTCCCAATT TGCAATTCCTTGGC
WI-4782	113 C	T	GATGCAGAAG ATAAAGTAGAA AATGC	GAACTCTTCTG GTATTTTCT GTTC	TCATTTGACTTTTGTAGAGTCTTCTCAGTCTTATGCTTATTTCTTTAGGAAAAAAGTCTAGGCTAGGAGAA CACAATTCAGGTCTCTCCAGATCAGAGAATACTAGAAAAATGC/TTGAAACAGAAAAAATAACCA GAAGAGTTCAATTAAGTTTCTTCCAGAACGATTAC
WI-4788	65 A	G	GCATAGAATC ATCTTGCTAAG ATCC	GGATAAAAT AAAAATTTGGC ATAA	AGGAGAGTTTGGCTCTTTTCCGGACTCTTGGAAATCAGTGCATAGAAATCATCTTGTCTAAGTTCCJA/G JTGAAAAAAAATTAATGCCAAAAATTTAAATTTATCCAACTTTAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTTCTTAAAGAGATGGCGTATCACTCTA
WI-5300	38 T	C	TCCAGAGAC CACTTCATTC	CTACTCTTCT ATTCATAATC CAAAA	CTTACTTCCAAAGTGTTCCTCCAGAGACCACCTTCATTC/CTTCTTTGGATTATGAAATAGAAAGAGT AGGTGTTATTATTCCTCTTTTACCAAGGTGAAATTTGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAAGTGACAGAGCCA
WI-4818b	121 G	T	TGATAATGGG GCCCTGTT	CCCTCCTTTTA TATGTATGCCA GA	TATAATGTTTGTTCCTAGTTGCCATAGACTAGGTATGTCACACATGAATAAACAATCTTATATA ATAATTTATCAAGAAGGAAATATACATATGGGTGATAATGGGCCCTGTG/TTCTCTGGCATA CATATAAAGGAAGGCTAA
WI-4818a	43 A	G	TTGCCATAGAC TAGGTATGTC AGC	CATATGTATAT TTCTCTCTG AATAAAT	TATAATGTTTGTTCCTAGTTGCCATAGACTAGGTATGTC/TA/GTACATGAATAAACAATCTTAT ATAATAATTTATCAAGAAGGAAATATACATATGGGTGATAATGGGCCCTGTGCTC:GGCATA CATATAAAGGAAGGCTAA
WI-5317	139 T	C	TTCCATTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTCCATTTTGTGTTGATCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAATAATATGATGTTATATTAACAATTTCAACTCAACAGGAATTCATTCTCTGGTAGCAGGT ATA/TC/TTGGACTCATTTCTCTTTCATCTATTTCTAGGTTATTTGCAGCCCCGAGATCTACCCAGG
WI-4888	56 G	A	GCAAGATATA AAGATTAAAG AAGATAACA	CAATTCCTACTA CCTCATTATT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAAGATAACAAGAG/ATGAAT AAATGAGGTAGTGGAAATGCTTGATAACTGGAGTAGTGCTT
WI-5328	44 A	G	---	---	AACATTTTAAACCATGCTACATTTACAAACACTGAAAAGACAG/AG/AAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATCTGGAAGGAG
WI-4897	93 A	G	---	---	GCCTTTTGTAGTTAAGCTTTTGTAGTGTCTTTTTTCCCCCACTAGGTACTCTCGGCCCAAT CCCCAAAAGAAAAAAGCGCTTGG/AG/GATAAACACATCTTC
WI-5345	29 G	A	---	---	CCCTGCTATAGGTCAGTTTAAAAATCCTTGA/CTGCTATGGTTGCTTGTGAGGCCACATCCACT GAGGTATATTCTGTCTGCTGCTATTTCTATATCACTCAGCTTTGAGATCCACTCCCACTCAACTTGCAG

WI-5370	143 T	AATAAGATGG TACCTTAACTA	CAAAGTTGGTA CAGAGAAATTTT AAA	TGCAATGTTACTTCTGGAAATCATAAAGGATCTGAGAGCCTACAGTATATGGCAACATTAACCAAT CTTTTGGAAATTTACCTGTATCCCATCATGGTTCAATTCATTTGCAAAAAAATAAGATGGTACCTTAACCTA ATAAAACAAT/CJTGGAAATTTCTGTACCAACTTTGCTTTTC
WI-9711b	423 T	A	---	GATCCTCTCATCCCTCTCCAGAGAGGAGAGGAAACACAAAGAAAGAACGCCTGGTGCAGAGCC CCAATTCCTACTTTCATGGATGAAATGCCAGGTGAGGAGACGGCTTGTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTGTAGTTAGTGTCTGCTATCCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTCGCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9711a	390 C	A	---	GATCCTCTCATCCCTCTCCAGAGAGGAGAGGAAACACAAAGAAAGAACGCCTGGTGCAGAGCC CCAATTCCTACTTTCATGGATGAAATGCCAGGTGAGGAGACGGCTTGTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTGTAGTTAGTGTCTGCTATCCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTCGCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9702c	345 G	A	---	GGAGGAATTCAGGGTGAATGGACTGCTCCGCTCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGCTGCTATTCAGCAATTCCTACTGCTATGATATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGTACAGCATCTGATAG
WI-9702b	344 C	T	---	GGAGGAATTCAGGGTGAATGGACTGCTCCGCTCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGCTGCTATTCAGCAATTCCTACTGCTATGATATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGTACAGCATCTGATAG
WI-9702a	179 C	T	---	GGAGGAATTCAGGGTGAATGGACTGCTCCGCTCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGCTGCTATTCAGCAATTCCTACTGCTATGATATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTTAACTTTAATGATCTCTGTGACTT CTTTTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGTACAGCATCTG
TGR- A003N21	49 C	A	---	TATAGTATTTAAGCAAGCTAGAGCAGGCTGTGGGTGGTGAATTTGGTTC/AJAGCATATCTTAGGT ATATAATACTTTGAAGCCATAACTTTAACTGGAGTGGTTGATTTCTTTTAACTTTTAACTTTGGA GGGTTTGGATTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTG TGATTACCTCTCAATCTATTGT
TGR- A004V30	203 C	T	---	AGAAATGGTACTTTCATAGGGCAGAGCAGCCACTTTTGGTAAATTTTAACTCCAAAGCTAATAAT AATCAAGAAGAAATAGAGAACATTAAACAAATAAAATTAATGTTCTTTTGGAAATACCTAATATCAG ATACCAACAGTACAGTGATAAGAAATAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAG/C/G,TJCTTCTAGGTTAGTAGAAAAAGTT

TIGR-A004W22	232	C A ---	---		GGATAATCAGTACAATAATGGGGACCTTAAAACTGCTGTGATGCAGGAGTGGAGGGCTGGGCAGTG CCCGAGGCGAGGAGGACAGTGGGACAAGGGATGCTCAGTGTGGAGCCACAGCCCTGGGCTCTGGGA TGGGGCATGGGAATGACAGGTTCCACATCATGCACAGAGGGGCTGTAGCTTGAGTCCAGACAG GCCTGCCACATTTGGTCTGCCCCCGCCCTA[C/A]CTGGAGATGTCTCTAAAA
TIGR-A005D24 b	138	C T ---	---		CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAATACTCTTTGAGATAATTGATTTTCATATTC TGTGGCTTTCAACCTCCATTTACCTCTTGTCATTTCCAAACATCTTTATAGAGAAATAAAAACCCAAATTT CT[C/T]TTCCACCATTTAGTTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCTATAAACTCTTCACTTAAATAATTAAAGGAAACAAT
TIGR-A005D24 a	123	A G ---	---		CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAATACTCTTTGAGATAATTGATTTTCATATTC TGTGGCTTTCAACCTCCATTTACCTCTTGTCATTTCCAAACATCTTTATAGAGAAATAAAAACCCAA TTTCTCTTTCCACCATTTAGTTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCTATAAACTCTTCACTTAAATAATTAAAGGAAACAAT
U03735	74	C G ---	---		TGAGTCTGAGCAGGATTCAGCAGGGCCAGTGGAGGGGTCTGGCCAGTGCACCTTCGCGGGCC GCATCC[C/G]TTAGTTTCCACTGCCTCCTGTGAGTGAGGCCCATTTCTTCACTCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGGTTCTGTTCTGTTGGATGACTTTGAGATTATTCTTTGTTCTCTGTTTGA GTGTTCAAATGTTCTTTTAA
U39840b	42	T C ---	---		GGTTGCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAT[C/CAACAGCAAAACAAAAACACA CAAAACCAACCGTCAACAGCATAATAAAATCCAAACATATTTTATTTTCATTTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTGATTCAAAATTCATTGTGTATTTACTACAAA GACGGCCCCAAACCAATTTTTTTC
U39840	56	A C ---	---		GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAATCAACAGCAAAACAA[C/A]CCACA CAAAACCAACCGTCAACAGCATAATAAAATCCAAACATATTTTATTTTCATTTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTGATTCAAAATTCATTGTGTATTTACTACAAA GACGGCCCCAAACCAATTTTTTTC
WI-8997	41	G A OCCC	GCCCCTTGCT	TGTTGTACGC AGTGCTCA	GTGGCCATCGATCTGGACCGTCCCCTGCCACTTGCTCCC[C/G]TTGAGCACTGCGTACAAACATCCA AAAGTTCAACAAACACCAAGAACTGTGTCTCATGGT
WI-7008	180	A G ---	---		TATACCACTTCCATTTGATGATGGAATGCTGCTGTTTCATGACCAACTTTATGGCTAGATGGTTCAGAA AGCACCAGTTCATGATAGGCAAGTTCAGGTCATATGTTGACTGATGACCCAGAGTCAAAACATTTCAG TTTCCACCAAAAGCCCAGTAACAGGCCAAGAGCTGTCTCTCAAAAG[G/G]AGAGTAGTTATCTGCAGA AGATGGCAGGGCTTGCTCCGAAAGCCTAGAGACCGCCACTGTGATTCACT
WI-9005	26	C T GGAATCT	CGAATTTGCTG	TCCAAAAGTC TTAAGAAGAA AAA	GGTCCCACGAATTTGCTGGGGAATCT[C/T]GTTTTTCTCTTAAGACTTTTGGGACATGGTTTGACTCC CGAACATCACCGCGCTCTCCTGTTTTTCTGGGTGG

WI-7593	46 G A ---	---	---	TTTTTGTGCTCTGGACACCCACTGCTCCAGGATGAAGGAGAGIG/AJAATGAGATCAGTTTGGACACTTCCTCTTGAATATAAAGAATCAACAAGTTACAGTCATGTTGGGACTTCTCTCTCTCCAAAGTGCATCTTGGGGAAGGCTCCAGTGTATCTGGACAGTTCCTTCAATTTTCAGGTGGGACTCTTGATCCAGAGAGAGAGACAAAGCTCCTCAGTGAGCTGGTGTATAATCCAGACAGACCCCAAGTCTCCAGTCCCTGGCTCTATGCCCTCTATCCTATCATAGATAACATCTCCACAGCCTCACTTCATTCACACTATCTCTGAAAATATTCCTGAGAGAGAACAGAGAGATTTAGATAAGA
WI-6962	78 A G ---	---	---	GCAGAGAGAGAACCATGCCAGGGGAGAGGCCACCCAGCCATC/GTGACCCAGCGAGGAGCCAACTATCCCAAAATATACCTGGGTGAAATATACCAAATCTCGCATCTCCAGAGGAAATAAGAAA:AAA
WI-7059	43 C G GCCATC	AAGGCACCCA	GGTCA	GATGAATTGTTGCAACTCTTAAAAAA
WI-9063	53 A C TT	CACTTCACTGA	TTCTACTTTCTG	AGCAGCCATCACATGATCTGTTTTTCACCACCTTCACTGAAGACACCATTTAT/ACJTACCCCAAGGGCAGAAAGTAGAACTTACTATTCATTAATGTTTGACACAAATTGGAATTGTC
WI-7079	293 T G ---	---	---	AAGGGGCATTGAGACTATAAAGCAGTAGACAATCCCCACATACCATCTGTAGAGTTGGAACATGCATTCTTTTAAAGTTTATATGCATATATTTAGGGCTGTAGACTTACTTCTTATTTTCTTTTCCATTGCTTATCTTGAGCACAAAATGATAATCAATTTATACATATACATCACCTTTTGACTTTTCCCAAGCCCC
WI-9074	38 A G AAAAG	GGTAAAGTT	GACAGATTTT	TTTTACAGCTCTTGCACTTTCTCTCGCTAGGCCCTGTAGGTAACCTGGGAT
WI-7104b	249 C T ---	---	---	TGGATGCCGAGGTAAAAGTTCTTTTGTCTTAAAGAA/GJAAGGAACTAGGTCAAAAATCTGTCCGTGACCTATCAGTTATTAATTTTAAAGATGTTGCCACTGGCAATGTAACTGT
WI-7104	249 C T ---	---	---	GGAGTTGCCCTTCTAAGGGAAGGAGATCTTATCTTCTGTTGGCTTGACCAGTCACGTTGGGA
WI-7104	157 C A ---	---	---	GAAGAGAGAGAGTCCAGGAGACCCCTGAGGGCAGCCGTTCTTCTGACTGAGAGAGGGAGGCC
WI-8974	34 C T AAGAACTCA	CCTGAGCCCTC	TGTAGGGCTGA	CCAGGCTGGAGCAGCATGAGGCC/CAGCAAGAAAGGGCTTGGGTTCTGAGGAAGCAGATGTTTCATGCTGTGAGGCCCTTGACCAAGGTGGGGGCCACAGCACCCAGCAGCATCTTTGCT
WI-9161	61 C T CCTGGC	CCTAAGCATTG	AGACTAGACA	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA/C/TGCCAGCTCAGCCCTTACACCAGTTTCCACC
WI-9014c	93 T C ---	---	---	TGGAGTTCAATGCAAGGGCAAAAGGCAGTGGCCATGCAAGCTGTTAA
				CTGTGAGGGTGAAGTTAGCATTACCCCCAACCTCAATTTAGTTGCCTAAGCATTGCCTGGC/C/TTC
				CTGTCTAGTCTCTCTGTAAAGCCAAAGAAATGAACATTCCA
				CCCTGTCCCATGCTGACCTGTGTTTCCCTCCAGTCATCTTCTGTTCCAGAGAGGTGGGCTGGAT
				GTCTCCATCTCTGCTCAACTTTA/T/C/GTGCACCTGAGCTGCAACTTCT

WI-9014b	44 C T ---	---	CCCTGTTCCCATGCTGACCTGTGTTTCCCTCCCCAGTCATCTTTCTC/TJTGTTCCAGAGAGGTGGGGCTG GATGCTCCATCTGCTCAACITTTATGTGCACGTGAGCTGCAACTTCT
WI-7023b	206 C A ---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAGACCCCTGCGTGCT CAGTGCCCTTTAAGTGCATCCCGCTGTGCTGACTTGTAGTGGATCAACATCTGCTACGGGTCCCC TCTTTTGGCCCCAGTATTCATGCGAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAC A/C/AJACACACATCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C ---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAG/A/CJCCCTGGGT GCTCAGTGCCCTTTAAGTGCATCCCGCTGTGCTGACTTGTAGTGGATCAACATCTGCTACGGGTG CCCTCTTTTGGCCCCAGTATTCATGCGAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAA CACACACACATCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T ---	---	CTGAAATCCCCCTCTCTGCCCTGGCTGGATCCGGGACCCCTTGGCCCTCCCTC/TJGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTGCCACCTCTCTGGCCCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAAGTTGTGTGAAGCAGAGAGAAAGCTGGAGGAAGCGGTGGGCCAAT GGGAGAGCTCTTGTTATTATTAATATTGTGGCCGTGTGTGTGTTGTTA
WI-9171	62 G A ---	---	ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAATAAAGAAAGTAGAGATAATAATCA[G/A] TTCTTTACAACCGATGGTAATTAAAGCTTGATTACAAAGACTTCATGC
WI-9174	47 T C T	TCTAGAGGTA TATAGGACAGG ACTG	GTGTGAGACCATCATGGTGCCAGCTAGGACCCCATCTCCTATTAT/TJ/CJAGTCCTGTCCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAAATTGAG
WI-7753	52 A G GAAGACAGA	CAGAGGTCTTG AAATACAGGG A	AAGGCCAGATGCACATCCCTGGAGGACATCCATGTTCGAGAGAACAGAT/GJATCCCTGTATT TCAAGACCTCTGTGCACTTATTATGAACCTGCCCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTCTTAAATCCATCCTGCTAAGTTAATGTTGGGTAGNA
WI-9186	76 G A CGCA	AAAGGAAAG TCTGACCTAGG T	AAAGAACTACAGAGGACGATGTCCAAACAAAAATGGCATCCTGTCAAAAATGGAGTTCCACT TCTCCCGCA/G/AJACCTAGGTCAGACTTTCCTTTTCATCTT
WI-9193	94 G A CA	AGAAATATTGT CTGCCCTAAAG TAGGGGG	TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTAGCAATTGACAGAGAATAA CTCAGAAATATTGCTGCCCTTAAGCA/G/AJATCCCCCTTACCACACACACCCCTGTCTC
WI-9015	48 C T ---	---	TTTGATTGATATCGTGAATCCTCAGCCGAGAAATGGGCTGGATTG/C/TJGCTTTGGTTAATACAT CTTTCCCTAAAGAAAGATAAACACAAATCCATTCCAGGTAGTCGGCACCACTAAGAA
WI-7254	37 A G AGGAGCCAC	GGAGTGGGTGT CATTAGGGA	GGAGCCAGGAGACAGCAGGGTCTGAGAGAGGAGCCAC/A/GJGTCCCTAATGACACCCACTCCTAGCC CTGAGGCTGTCGCCCTCAGACTGGGGAAGAGTCCAAAGGAAGGAGGAGGCCACTCCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG



WI-9231	32 G C	CAGGTCCCA GATTGA	CAC TTGCCCAC ACTCAGAC	GTGACCCCTGTAGGTGAGGTCCCCAGATTGA[G/C]GTCGTAGTGTGGCAAGTGTGTCAAAAGGGGC TGCCCCCAGGAGATGAGGCTGAGAGCAGGAGTGTAGGCCGGAAGTCA
WI-7836	120 T C	CAAAATAACA ATGCAACGTT C	GCTCTCAGAC CAAGATTAGA AATC	TTGTTTGGGAAATAGAGAGTTGAGATAAACACTCTCATTTCAGTAGTTACTGAAAGAAACTCTGCTA GAATGATAAATGTATGTTGTTGTTCTAACTCCAAATAACAATGAACGTTCC[C/G]GATTTCATAAT CTGGTTCTGAGAGCAATTTGGTTTCAGTTGAGCAATCCCATACAGCT
WI-7286	65 T C	CAGCTTCAGCT TAACTGACAG A	AAACAATCTA ACCAGAAAGCT TTAA	TCCATTCTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTCAGCTTAACGTGACAGATTC GTAAAGCTTTCGTTAGATTGTTTTCACCTTGGTGATCATGCTTTTCCATGTGTACCTGTAATATT TTCCATCATATCTCAAGTAAAGTCA
WI-7858	91 T G	CTAAGCATGT ACGTGAATTT TAAAT	CCCAATTTTA TTAAAGTTTA CATCTAT	CAAAATCTTGGAAATATCTCAATGTTAATAACAATATGAATTTTCTCATGCATACTATTACTACT AAGCATGTACGTGAATTTTAAATTTGTTATAGATGTAAACCTTTTAAATAAAATTTGGGTGTGG
WI-7860	50 C G	CGTACCTCCAA ACATAATTGA TTC	---	GAAATTAGGGAGGGTGTCTCTGTGGTCTCTCCCTGCCCTCTCCCCA[C/A]GTGGGGAGAGACC TGTGATTTGCCAAGTCCCTGGACCTGGACCACTACTGGCCCTATGGTTGGGGTGGTAGGCAGG TGAGCGTAAGTGGGAGGGAATGGGTAAGAGTCTACTCCAACTAGTCTCTATGTCAGACCAG ACCTAGGTCTCTCTAGGAGGGAACAGGAGACCTGGGTCTCTGGAT
WI-9064	29 A G	CGTACCTCCAA ACATAATTGA TTC	GCTTGAGTGTA AGTCTCGCAGA	CAAGCGTACCTCCAAACATAATTGATTC[A/G]TATCTGCGAGACTTACACTCAAGCAATCCTGAGG AATACTGAGGAGGGCTGGTACTGCTCTCTGCACTCTGCTGCTTTG
WI-7307	128 G T	---	---	CACACTGTCTGTTCTCAGTGTGAGTCTGCGAGGTGCGAGGTGAGGTGGGTAGCCGGGTTCCACA GGCCCCAGCCCTGGCAGGGTCTGGCCCCCAGGTAGGCGGAGAGCAGTCCCTCCCTCAG[G/T]AACT GGAGGAGGGGACTCCAGGAATGGGGAATGTGACACCACCATCTGAAGCCAGCTTGACCTCCAGT TTGCACAGGGAATTTGTCTGGGGCTGAGGGCCCTGTCCCCACCCCGCCC
WI-9274	25 C T G	GAAATGTGAC TTCACTTGGT G	CAGGTAGAATT TTCGTCCATT G	GAGGAAATGTGACTTCACTTTTGGTG[C/T]CAATGGACAGAAAATCTACCTGTGCTACATAGGAGAA GTTTGGAAATGCACCTTAATAGCTGGTTTACACCTTGATTCGAGGTGGAAA
WI-7313e	266 T C	---	---	AATTCCTTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAACTTAAAT TGTTTGCAGCTTTTATGTTTATATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTAT AATTCAGCCAGTATCCACCAGTTTTGTTTATGTTTAACTTAACCTATTATCTCTGGATTTCATG AAGTGTAAATATCGTTTTTTGTTAACTGAATAGAAATTGTATAGCGATGA
WI-7313c	256 C T	---	---	AATTCCTTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAACTTAAAT TGTTTGCAGCTTTTATGTTTATATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTAT AATTCAGCCAGTATCCACCAGTTTTTGTGTTATGTTTAACTTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTTTTGTTAACTGAATAGAAATTGTATAGCGATGA

WI-9281	68	G A ---	GCTAACACATTT TTAAACCCGT	CAATTTATTTG AAAGCTATTCA GACA	--- GACA	ACTGGTGGGAGACTGTGAGGATCCAGGATTCAGTATTCCTGGCCACAGAGGGCCTTGCTGGCTACTGG [G/A]TGTAGTTTGCAGTCTGTGCTTCCCTCTCTTATGACTGTGTCCC
WI-7848	142	A G CTC	GTATATTACA ATGATCACCG	CCACACAGAAC TATTGTAAAC	--- AA	TTCTGAAAATATAACAGCCATTGAGCTATTTAAACCTTGTAATTTTTTAAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTCGTGACAAATAAAACATTAAATGCTAACACGTTTTTAAA ACCGTCTC[A/G]TGTCTGAATAGCTTCAAAATAAATGIGAAATGGT
WI-9304	70	G A ACTGA	GTATATTACA ATGATCACCG	CCACACAGAAC TATTGTAAAC	--- AA	TCACGTTTGGTGCTTCTCAGATTCTGAGGAAATGCTTTGTATTGATATTACAATGATCACCGACT GA[G/A]AATATTGTTTACAATAGTTCGTGGGGCTGTTTTTTGT
WI-7933b	314	C A ---			---	TTACAGAACTTGGCCTGTGCCTGTGCTCCCATGCTAGGGCGGAGGGGTCTTTTCCTTCTCTTTCC TAAGTACCCCTTTCTCTTGGCCAGGGCTGATCCTACCTTCCCTTGTCCCTGGGCTGGCTGCAC AGAGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATAGCAATTTAGTATTGTGCACAA AGTCTAAGGGACCATGGCTGCCTGCCTTGGGGAGGAACCATAGCTCCCT
WI-7933	96	G C ---			---	TTACAGAACTTGGCCTGTGCCTGTGCTCCCATGCTAGGGCGGAGGGGTCTTTTCCTTCTCTTTCC TAAGTACCCCTTTCTCTTGGCCAGGGCTGATCCTACCTTCCCTTGTCCCTGGGCTGGCTGCAC CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATAGCAATTTAGTATTGTGCA CAAAGTCTAAGGGACCATGGCTGCCTGCCTTGGGGAGGAACCATAGCT
WI-7374	182	T A ---			---	CCAGATGTGCCCATCAGTTTCTGAGGCTTTTGTACTTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTGACTTTGTAAATATTTGAAATGTAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTTGAACCACTTCTAGCTGCTGTGAAGAATATATTG[T/A]CAGAAACACAAAGGCTT GAT
WI-9343	78	C T CCTCTGCCA	CCAACAACAT CCTCTGCCA	AAATGAAACTT ACGTTTGTGTG TG	---	GGTCTGCTCCTGCTACCTTGACCTTCCCTTCCCTCTCTCTCTCTCATCATCATCCCAACAACAT CCTCTGCCA[C/T]ACACAACAACAAACGTAAGTTTCATTTGGGCAAA
WI-7386b	104	T A ---			---	CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAACAATTTGTTA[T/A]GTGTTTAGAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75	A G ---			---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAAACCTGGAAGTTCACTTTTGTATTAT GCTCTT[A/G]TATTACAGACTGATGCCAGACAACCTTGGGAAGA
WI-9360	79	T C TTGG	CTTTAGAAAA TCTGCTTTAAC	CTTAGGGAACA CAATTAGAGGA A	---	TGAAGGGGTGTGGCATCTGTGTTTCTGATGCTTACTACAATATGTAACCACTACTTTAGAAAAATCTG CTTTAACTTGGT[C/J]ATTCCTCTAATTGTGTTCCCTTAGGAATGACTGTCCCAAG
WI-7423	107	T C GTTC	TGCTGGGCTGT	GGTCCAGAAGA GGOOG	---	TGCTCCCTGTCCCATCTGCAGTGGACCCAGGACCCCTTTTGGAGGTGGGGTGAAGTCTCCTT GGCAGGGATTGTGACACTGCATTGCTGGGCTGTGTTCC[T/C]CGGGCTCTTCTGGACCTTGACCCGTG GATACCAGGCCATGTGCCATGGTATTGGGTCTGGAGGGTGGTGAATAAAGGCATCTGCT

WI-7424	131	T A	CAAGAGAGAG AGAGGAAAGA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGGGAGAGCAGAGTTAGAGAAAAAAGCCACGGAGGAAAGG AAAAAACATCGCCCAACCTAGAAACGTTTTCATTCGTCATTCAGAGAGAGAGAGGAAAGAAAA T/AJACAACTTTCATTCCTTCITTCACGTTTCATAAACATTCATACATA
X86400	118	A C		---	TCCTGCAAGAAGTTCTCAAGCCTTTTGAITTTTGTCATTAAGTACAGCTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACTTCTCTCAATTTAAGTGAGA/CJCTCTTTTAAACACCT GTTAAATTTAATGTAGCAGCTGAGAACTCTAAATATGTAACACTCGTTATTTGTTCAITCATCCA TCCCTTTTCCCATGAATATTCA
WI-8053	242	T A	---	---	GTGGCCACTACATGTTATAGAAACCATCATCTTGTACACAGCAGCTCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAAAGCATTAAAAGTGTCCTTAAAAGGGACTTTTAAATCAACCTAA TAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCATTTAATACATGCTGAAAAGGGTCCACA ATTAATCTTTGATCTTTTACTCACTGTTAACTTATATAIT/AJTTCAGAAC
WI-6190	165	G A	---	---	TACACAATGAATTCCTTTTATTCGGTATGCATCCACATTTAGTGCTCTGAACAGCAAG TGAAAGACGCGCAGCAATTTGCCAGGAGGTCAAGCCACCAATTTCCGGGATCTGCTGTGCACACCGG GTTCCCTTCTTAATCCCTGCTGAGGATCTTG/GA/JAAGCAGCAGCAGCACCACCAAGGCATGCA CCGGATTCAAGGTTCTTTTGTTCAGTTGTCAGATTCCAACTAGACCCCA
WI-6275	148	G C	---	---	AACAGTCACCACCAACCATGACAACTCGCCAGGCAAGGCTTGTCTCCCTCCCTCTCTGCTCCC ATGTGCTAGTCAGCAAGGTGGGGAGGCACCGATGTTAGCTTCGCCCAAGGGAGTATTACAGAGA GAGGCTTGGGAAA/GC/JGGAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAACTG ATTTGCTTTTCAGTAACGGTATGCTGAA
WI-6421	41	G T	---	---	ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTGTGATTGT/GJGGGCTTCCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGGAAACCGTACCTGAGAGGGATGGGGCTCTCTCACA GAATATTTGGGGCAGAACCTGGAACCTGGCCACCGGACATCCCAATATCCCTCCTCCTCAGGG CTCACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215	T A	---	---	GGGTGAGACGGGTTTATTGTGCACATTTACACAGCGTCACAGCTGTGGGCTGGCAGCGGCCATGCTC CTGTGGTGGGCTGCTCTACAAAGGGCTTCACTTTTCTTCCACACACTATGTACAGTCAGTCTCCAA GGTGATGGGCTACAGTGTGTCATCAGTGTGTGTACACACATTTTACATAAATTACACAGGACTC ATACATGAAAAAT/AJAGAGCCTAAGGGCCTGTATTTTAAATGAGAAAAAA
WI-9420	202	G A	---	---	AACTGTTTACAAAATAGGCTTTGCAAACTTCACTACTGAATGTAAAGTCAATGACTGTGTTT TAAATATGTACCAAGGAAATACAAATGGATAATGATCAITTTTCTCAGGAGAGAACAGCAG AGAAATAAGGATACTGCACAAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG [G/A]GCATTCCTTCTCACCTTAACCTGCAGCTGTGCAAGATGCCCTCAGTGTG

WI-9448	184	G A ---	---		TGGGGCTGCTTTAGACTTCATTTCTAGAGCAGAGCACCTAGTAGAGAGGAATACCTGGGAGAGAGAC TGCTTGCCCATGGTGGTTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAAATGGGCTTGTTCCAAAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCTCTGGCTGGATTATCCAAAGCGCATGTTCTTAACGTGCCCGTGAGCAG
WI-9470	204	G A ---	---		ATGTCAAGAGACACAGACAAGGAGTTTTCCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTCCCTAAAGCCCCAGATTCTTACTAGAGCCGCTGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCTCAAGCTCACCAGGGCTCACCTTCCCAAAG
WI-1245b	201	G T ---	---		GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCCTCATAAGGAAGAGTAGGTAAATGGCA TCCTAGGGCAATGGTAGGTGCCTGATGCAGATCTGCTGTGAGCCATGTCTGGCATCACAGGGTGGT TTATTAAATTCATTTATCATCTGGACAGCCCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC[G/ TCTAAGATCCCCAAGGTGGCTCTGTATCCAGAAA
WI-1245a	85	T C ---	---		GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCCTCATAAGGAAGAGTAGGTAAATGGCA TCCTAGGGCAATGGTAGGT[G/C]GCCTGATGCAGATCTGCTGTGAGCCATGTCTGGCATCACAGGGGT GGTTTAAATTTCAATTTATCATCTGGACAGCCCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCTGTATCCAGAAA
WI-1031	149	G A ---	---		TTCAAGTAAAGGACAGGCTAGAACAAAGCGTTCCCAACCCCTGGCACCATGACAGTTTGGACCAAA TAACTCTTTGTTTACAGGGGACTGTCTCTACACATTGTGGATGTTTAGCAGCTCCGTTGGCTTACCCA CTAGATGCCAGCA[G/A]CACAAACACCCCTCCCCAACAAATCATGACAAATGAAATGTCTTTAGACATT GCCAAATATACCTTGTGGGACAAAATGGCCCCCTGATTGAGAACCCACTGGTT
WI-5385	110	G A ---	---		AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAATGGTGGGATTGAAAGAGG GAAGTCTCGATAATTTTAAACATATGGTTTCTTGGCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCITTTATCAACAGACTCTTTGAATCAATTTAGAGATACCTCAGTGACCCCATGGCTAGAGTTCCCTGAC CCCTGCTACGGGAAACATTGAATGCA
WI-5403	199	T G ---	---		ACCAACCCTTGGCAAGGCTCCCCAAGACTCACCACCCCAACTTTGGTGCTTACCCTATG:CGGGTG GGATTGAAGAAATAACCAATAATAATTGCTACAAATTTCCAGTAGTTACCAGGCCACCCAGCCTAT TGGAAGAAATCATAAATGTAAACCCTACAATGATTGCTCTCTGGCTGGTGCCAGGCATAGAGTT/G JGGCTACAACCCCATTTTATCATTGAACCCCTCAGAACGATCCAGTTGGGGCT
WI-5801b	157	G A ---	---		TGGTATTTTCTTTCTTAAATGTTATGATTAAATAGTGCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAAGAAAATAAGATATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]AGGGAATGAGAAAAGCACAACCCAGAAAAAAGTGTGT GGCTTAAGGGAGCCCAAGGAAGTTAAGT

WI-5801a	48	A G ---	---	TGGTATTTTCCTTTCTCTAAATGTTATGATTAATAGTGTCTTTGTA/G/GAAATTTGAAAAAATGT AAATCAGAGAACAGAAAGAAAATAAGTATAGTTGAAACCTCTAACAATTTTAGATTTTAAAGGCC TAGGAAAGAAAGAGAGCCTGGGAAGAGGGAATGAGAAAAAGCACAAACAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAAGGAAAGTTAAGT
WI-5696	61	C A ---	---	TTCTATTTAAATCCTGTGCCCATTTGCAAGACTGCATTCAGTCTGCATGAGCCTTAGTTTC/A/TAA AAGCCCCCTCACACCGAGGGGACAATGTTCAGAACTAAATGACTGCAGGTGAGCAATTCCTGTATTA TACAAACTGGGACCAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGGGTGAGTTTATTTAAGCTT
WI-7461	153	C T ---	---	TATTACTAGGTTTCATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTTCTAACGCTCCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCCTG TGGCAGGGACTGTGCTC/TGTTCCCTGTTGGTCCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTCTGCA
WI-9716	221	G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAACTCTGAGGCTTTAATGGTCCCTGTCTCTAAC GCTTTTGGTACTTTCTCTTCTGAAGACCAACCCCTTTCAAACCTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTCAGATGTGACTTCTCTACATTCGAAAACTAGATGAGTTAGGCTCTCTTCATCT CAATTGAAAAATCTAGAA/G/A/AAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49	C T ---	---	TTTTCGTTAAGTCTTGTAAGCCACACAGAAGTATCTACTCTCTTTAC/C/TAAAGTGTACTTTGCA TATATTTATGGGATGATTCATCCCTACTTAAGATTTTCTCTCTCAGGTTAAATATCCATTTCCCT TTGTCAGGAGTTTCTAATTTGGCCTTCTTTCTAAACCCCTAACCAATTCCTGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31	A C ---	---	GAAAACTCGTTGGCTCAAAGGAAACTGTAG/C/AAATCTTTTTTTTATTTTGTCTTTTAACTC AAAGAGTGGAGTTTGCAATTGACCTTGATGGCAGCTGCTCTTTGTTTGGTGTAAATCCCTCTAGT GGGCACTTTGCAAAAGCAATTTTAGAGCAAAAGGTGGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAAG TAGCAAAATGGAAGAAAGGTTAATGGA
WI-10312	41	A G ---	---	AAGGCCAGTGGGAAAAGCAGACAAAACACTCCAAAGAAATAC/A/G/AGATAATAAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTCTGCTGATGAGGGCATGTGAGCCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGGTGAGTCTTGCCAGTCCCATAGTAGGTGTTCCATAAATAAAC AGTGACTAACTGAGGTAGATCACAGAAGAAATTTCA
WI-11152	179	C T ---	---	GATTCCTTGGCAGATGCAGAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAAACGAGCCCTA ATTTCATAGAAACAGACTCTACAAAGGACCAGTTAAAGGTCTCGCACCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAAGTGGGACAAAAGGCTTGTCA/C/TCTGTGACAAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167 A G ---	---	TGGTGAGGAGCTGTAAAGGCTGAAGAATAGTCTCTGCTGGTCTTTGTTGGAATGGATGAGTCCT TTTACAAAATTTTCCCTTGCCATGGGTGTTATGTTTAGAATCATGGAGTTGGAAGACTTAGATTCA ATTTGGGGCTGTACAGTTTACTGGAAGTTG[A/G]TGAACCTTGAGCAAGTGCTCTTAATGTCCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198 G A ---	---	GGGTTCAATTAACAGCTTCCACTGGGTCTCAGATTGACGGAGATGTAAAAATAGGAAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACAACACATTAAACTCCTCCCCACICTA CCCGCCAAAGTCTACCTTTTGTTCTTTTATTTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A] CCATGTCATTTTTCAGAAAAGCAGTATA
WI-4823	164 C A ---	---	TTTATCTTTCCAAACCATGTGTGTTTCTTCACATACCTTTACGTAATTTTAAATCATGTCAATTAATTA TGCACCTACTGTTGGCTACGACATGCTTCCAAATTTGTAATTTCCCTAACACAGCAAGCATAACT GATGTGCCATCTTTGTATTCTCTAAAC[C/A]AAAGAAAAGTGCTTTTGTGTCATCTGCCCTCTCTGT CTTCTCTGTTTCACCTCTCTGTAATTTCCCTATTTCAGCAATTCATGATTA
WI-48	72 A G ---	---	AAAAACAACCTTCATTTGACATCTAAGAAGATAAAGAAAAACAACGATCCACTGTGTGTTGCTT GATTT[A/G]GGAGATAAAACCTGATCTCTAAGAAAATTAACCCAAAGCAGTACACTAAAATAGCCT TTGTGTGGTTTTCAGGAAAGAAAGCCAAATCCAACTAAGTTGCTAAGAAAAATATGTTTCATATCA CTCTAACTTCCACATAGAGCAATTAATAGCA
WI-9705	111 C A ---	---	TGAAAGGACCAGTTGGAATGCCTACCAAGGTAAAGTAAATCGAGGGGGCAGGAAGTAGGAGTTGCTT CCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCGGTGCC[C/A]AAAATTTGTTAACACTGATGC TGCTACAAACGACATAGAAATCGGTGTAGATTGCGGTTCTTAGTAAGTAGCTAATGTTTAGATA TGATTGTGAATTAATGTTGCTGTGTTCTTGGTG
TGR- A004Z48	177 A G ---	---	CAATAATCTCTGCTTGAAGTTGCTTAGGGCCCATGGATTTCATGAAGGTGGGGCAGGTGGACTG AAGATCTGTTGGCAGGCTCACAGACGGGGTGAGGGGAGAGATCGTGGTTTCATGAGATCCCAT CTTGGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGA[A/G]TCCTCCAAATTCAGGGGCTCCC GTGGGATGGTGGAGCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
U17579	34 T G ---	---	GGGATTCATGTGTCTCTCATCCAAATAGCACTT[G/C]ATGACCTCAGCCCCATCTTTCTTCCC TATGTTCCAGAGACAGAATAGACCTGGCCCTTCTCTAGGGGATCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC TGGGGAGAGGGATCTTTCTAGTTGA
WI-7747b	88 T G ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCTGCTTTCGTTAACTGTGTATGTACATA TATATATTTTAAATTTGATTT[G/A]AAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTCTGTTGTTGTTGGTATCCTGCCAGTGTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTTACCATTGTAAATAAGTATATAATTTTTTATGTTTGTCTCTGA

WI-7747a	44 T C ---	---	---	GTGAGCGGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGCT/CJTTCTGTTAACTGTGTATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAAGTT ATTTCTGTTTGTGTTGGGTATCTGCCAGTGTTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTACCATTTGTAATAAGTATATAATTTTATGTTTGTCTCTGA
WI-7189	197 T C ---	---	---	TCAGAAATTTCTCTTCAGCTCATTTTGTCTCTCTCAATTAAGGGAGTAGGTTAAGTGAAGGT CACATACCATTAATTTCCCTTCAACAATAATAATTTTACAGAAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGTTATTTTATATTAAAGCCTACAAACATTTT/CJAG TTTGCAATAGAACTAATACTGGTGAATAATTTACCTAAACCTTGGTTAT
WI-7850	57 G A ---	---	---	AGCCCCAGCTGGACTCATGGATGTGCAACCCTTGTCTCCCTGCTCTTCTGCTCTGG/CJCTCATGTA TCTGGCAGCTCTGGTACCCCTCTGTGGTGCCATCTCTACCTCTGACACAGACTGCCTGCCTTGAAGCT GAGAAAGCACAGGGCAAGGAGCCAAAGGACCACAGAGCCTCAGCCAGCCAGGATCCGCTCCTCATTTT ATTGGTGATGATGAATGGGAATGAATCAGGGGGCTGTCTACTAGAGCC
WI-7907	69 G C ---	---	---	CTCTCTCTTCCATCCCATACCCCTAAATAGGTCAGGTGAGGGAGGCTGGGAAGAGGTGGGAGGAGG G/G/JAGAAAGTGAAGGAAGATAGGAAGGATATTACCTCTCTCTGTTATTTTAAAGAAACATTTGTTT GGTGGCAGCAATCTCCCTGTCCCTATCACGTGAGAGGCCCTAAATTTATATCTATAAATA1.ATTAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAATTTATGTCAAAGTTTAAAT
WI-7919	242 T C ---	---	---	GAAGGCAGCTGGATCACCTTCCCGAGTCTTGGGCAGCGCTTGTGTGAACACGAGAGCTCCTCCT CAGGGGCTGGCAGTCACTTCTTCTGATGATGATGATTTGGTTAAACACTGTCAAATAATAGAGAT GTGCCAGATTTAGATTTCTTACCCCTAAATCTGTTTAAATTTGTAACCTTTATCCATTTGAAAGTGCA AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAAT/CJACAACTTT
WI-7928	101 T G ---	---	---	CTCCCTTCCATGTCTCTCAGCAGCACGTTGGGGCACACTTGTTCATCTCTGACCCTTGTGGGCTA TTCCCTGCGAGTGCAGACATCGTCAAAATTCAT/GJACAAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACCTTAAAACTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCAITTAATAAATACGTACATTTTCGAGGTAATGGTA
WI-7936	131 T A ---	---	---	TTTTGAGTCAAGACTTAAAGGGCCCAATGAATTTATATACATCTGCATCTTGGTTATTTCTGAA GGTAGCATCTTTGGAGTTAAATGCACATATAGACACATACACCCAAACACTTACACCAAAC[T/A] ACTGAATGAAGAAGTATTTGTAAACCAGGCCATTTTGGTGGGAATCCAAAGATTGGTCTCCCATATG CAGAAATAGACAAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99 T C ---	---	---	TACAGTTCCAGCCCGTTGCCCACTCATCTGCGGCTTGTCTTGGTGGGGGCGAGATTGGTTGG AATGCTTTCCATCTCCAGGAGACTTTTCATG/CJAGCCCCAAAGTACAGCCTGGACCAACCCCTGGTGTG TGAGCTAGTAAGATTACCCCTGAGCTGAGCTGAGCCTGAGCCAAATGGGACAGTTACACTTGACAGA CAAAGATGGTGGAGATTGGCATGCCATTTGAAACTAAGAGCTCTCAAGTCA

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WI-7805	101 A G ---	---	---	TTTCTAGGCTGTACAGTCTGATGCATGATTTTTTTTATAAATATTTTCATCTCTTGGAATTTGGATCTT TTTACTTTGAGCATATATTTAGAAATATGTGTG/GTGTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGCAGGTTTCATTTGGAATAGTTTAAACAGTCAGGAAGGCTAAACTGGTCAGTATTATGTGTAGC CCTACCAAAAATAGCCAGTAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---	---	---	GGCCAGGAGATTAGCAACAAGGATTCATCTGTTACTTACTTGGCCCTTTTATCTTTCCCTCTTGCCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGTCTTGCCAGTGTCT [G/T]CTACTCCTCAGGTGCAGCATACATAACCAAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTGGCAAAATGTCATCAG
WI-140	252 C T ---	---	---	ATTTGAAGATTGGAGGGCTTTGCAGAGGAAATAGATTTCAATTGGATCCCCAACTATAATGACA AGTTTTAAATTAGGTGTGATCAAGGCTTCTAAAGTGAATGCAAGTTGTACCAGTAAAGTTTATA TCTCCATTCAGCCAGCTCATTTGCCAGAAAATTCAGGTGAGTGGATGGCCAGACTATCTGGCAAG GATGAAAATTTAGTTTAAAAATGTGTCATTTGTCTGTATTGGCATTCCTT[C/
WI-198	218 C T ---	---	---	GAGGTCTTTACGCAACATGGAAGCCCTACTGCTCAACCCCGAGTTCGCCGGATCAAGTGTGGCACC CATGATGGAAACTCTTGCCATGGTTTTAGTACCCCTGGACCAAGTAGTCAATCCATCCTGACTTTAAAA TTCTAAAGCCCTTGATGGGACAATCTCTGCTAAAGACTAACCACTTCCCTTATCTTATCTTCAGCTA CCTGCTTCCCTT[C/T]GTTTAAACAAGCATAGAAATATCTGAACAAC
WI-205c	146 T C ---	---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTGT/C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTACCTAAGAAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCCTTTATTTTGTAGTTCCC
WI-205b	146 T C ---	---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTGT/C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTACCTAAGAAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCCTTTATTTTGTAGTTCCC
WI-234	165 G C ---	---	---	GAAGACTGAGTTTCCAGGAGTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTC AACCTGTTTGC AACCCAAAGTNC TTTCC AAGAGG TCTCAGACTACCTCCTCCATCCTCCCT CTCCCCACAACACACAAAATACAGAGATT[G/C]AATTCAGGAGCCAGTTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTCTTTAGTTTCTCAATGGGAAATGG
WI-276b	25 A G ---	---	---	AGCTTTTGAATCCAAAAACCACATG/G]CTTGACTCTCTTATCCTCCTCTTGTGTAAACATCTATCC CTGAGGCAAGAAAATACAGAACACCCCTGTGGCTGCCTGAACGGAGGAGGATGGGGGGGAGACAT CGGTCAATGTATCAAAAGCATCTCTGCTGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTTATCTCTCTGCTATCCCTGATGACTGGGCAAA



WI-276	25 A G ---	---	AGCTTTGAAATCCAAAAACCACATAG/CJCTTGACTCTCTTATCCTCCTCTTGTGTAACATCTATCC CTGAGGCAGAAAATACAGAACACCCCTGTGGCTGCCTGAACGAGGAGGATGGGGGGGGAGACAT CGGTCAATGTATCAAAGCATCTCTGCTGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGTCTTATCCTCCTGCTATCCTGATGACTGGGCAAA
WI-427	59 G A ---	---	TTTCCCAATCCACAGGTAAACTAATAATGGATGTATAGAAATTTAGAACTACTTCC[G/A]GTTT TTTCCCTGGGAAAATATTCACAAAACATTTGTGGCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTCATCAGACAGGTAGAGGCCCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCATTTATTAGAGCCAGGGCTTGCCTGTCACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTTAA[T/C]AAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTTAA[T/C]AAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTTAA[T/C]AAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---	---	GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAAAC TTGATCTAATATTCTTCAACAATAATACCTGAGAGAAATAAGTCTATTAAAT
WI-597b	141 A G ---	---	GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAAAC TTGATCTAATATTCTTCAACAATAATACCTGAGAGAAATAAGTCTATTAAAT
WI-597	136 A G ---	---	GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GAT[A/G]CATGATAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAAAC TTGATCTAATATTCTTCAACAATAATACCTGAGAGAAATAAGTCTATTAAAT

WI-611	66 G C ---	---	TTCAAAATTAACACCATTTGGGTATATTATAATTTNGCTCTATCCATAGTTCTAACCCCTCTTCTCT[G/ CJACAGTGAGACACCTGCTTCTATTTGCTTACGTATTACGATTTCGATCAGTCACCCATCTGGA ACCAAGGTTTCATTTCTGCTGACCCCTCCCTCCTCACCTACTTGGGCTGCTGACTTCTCTTCTGGGCT GAACCTTCTCTGTGGCTGTCCGGCTTCCCTGCTTGGGCTCCAATAC
WI-681b	156 A G ---	---	TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCACCTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATT[G]TTATACCTATGGCACCACTTGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCACAATCTGTCATGGTTT
WI-681	156 A G ---	---	TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCACCTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATT[G]TTATACCTATGGCACCACTTGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCACAATCTGTCATGGTTT
WI-867b	119 G A ---	---	AATCTTAACAGCCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[G]AJTTGTGTTTGGC CAAATAATATCTCCCGCAGGACGTCCTCTTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGTATGTTTGAATGTGTCCTCCCAAGCACAATCTGAAACTTA
WI-867	113 A G ---	---	AATCTTAACAGCCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[G]AJTTGTGTTTGGC CAAATAATATCTCCCGCAGGACGTCCTCTTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGTATGTTTGAATGTGTCCTCCCAAGCACAATCTGAAACTTA
WI-867	119 G A ---	---	AATCTTAACAGCCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[G]AJTTGTGTTTGGC CAAATAATATCTCCCGCAGGACGTCCTCTTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGTATGTTTGAATGTGTCCTCCCAAGCACAATCTGAAACTTA
WI-871b	123 C G ---	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCACAAATGTAACCTTGTCACAAACGA ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGCACCCACCTACCTCATG[C/G]AACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGCTGTATTGTACATAA
WI-871	123 C G ---	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCACAAATGTAACCTTGTCACAAACGA ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGCACCCACCTACCTCATG[C/G]AACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGCTGTATTGTACATAA

WI-884	198 T C ---	---	---	AGGTTCTGGACTTGATGCTGGGAAACAATTGGGTGNCCTGGAGAAATTCCTATTTTGGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTCTGATCTATTGGGA ACTTCCCTCCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATAITCIG ATCCCGCATGCAACATTTATTAGTGAAACATGATGAAAATGAACATAAT
WI-921b	205 G A ---	---	---	CACITCCCAAGGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTATCTGG CAGTGATGCTCTCACGCTGCCCCCAAGAAAGTCTTNGCCAGGAAAGACGATCCATCTAC TCTIGAGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTCTCCGAG
WI-921	205 G A ---	---	---	CACITCCCAAGGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTATCTGG CAGTGATGCTCTCACGCTGCCCCCAAGAAAGTCTTNGCCAGGAAAGACGATCCATCTAC TCTIGAGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTCTCCGAG
WI-945c	90 G C ---	---	---	GGCTGGGATGAGAGGTCTACTTGTTGTTACTGGAGGTTTCACTGGCTTGTGTAGAACTAGNAAAAGNA GAAAGAGACAGNGATTGGCTAACG/C/CATGGCAGTAGTGGCCCCAAGGCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAAATCTTTAAAGGGAAATCATGACAGATTTCTTGGCTTTA
WI-945b	90 G C ---	---	---	GGCTGGGATGAGAGGTCTACTTGTTGTTACTGGAGGTTTCACTGGCTTGTGTAGAACTAGNAAAAGNA GAAAGAGACAGNGATTGGCTAACG/C/CATGGCAGTAGTGGCCCCAAGGCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAAATCTTTAAAGGGAAATCATGACAGATTTCTTGGCTTTA
WI-960b	167 C T ---	---	---	TTGCTTCAAAGAGTTCTTGCTCAGGAAGTTATTCATTGAGCAACCTAAATTTTGTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCTTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 G A ---	---	---	TTGCTTCAAAGAGTTCTTGCTCAGGAAGTTATTCATTGAGCAACCTAAATTTTGTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTACC CTGAGGAATTTATCAAAGATG/A/TTAAGTTATCTTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 T C ---	---	---	TCCCACTGAGTATGGCTTTCAGTAGTTTATTATGATGTCCTAGGTACATTTGTTTATTGTTCTG CGAATTGTTGATTACTTTGGGAGAAATGCTCAACTATATAATTTGCTCTGACCCCTTTCTGTGTTTC CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCACTA/C/C/GCTGTTTTTACTCTCCTCTG ATTTTTTTTCCATTATTTTATTGCTCTGGCTTCATTTTGTAATNTG

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WI-1147b	204 G A ---	---	---	TTGGCCATTATTTGAAGATAACCCACACCTTGGTGTCAGGGTTTCACAGGTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCAGCCACCGCAACTTCTCCTCCCTGGCTC CTGAGCCAAAACAGGCATTTACCATAAATCACTTTGTTAGGATGAATATCTGGCCAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
WI-1158b	147 C T ---	---	---	GCATTGAGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGCTATGTCAGGCCCTTGGTTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT TAAGTGTGGGG/C/TJCTGGGGTCAGGCTGCCCTGGGTCAATCCTGGCTCCAACTGCTTTGCTATG GCT
WI-1158a	124 C G ---	---	---	GCATTGAGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGCTATGTCAGGCCCTTGGTTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT GGCTAAGTGTGGGGCTCTGGGGTCAGGCTGCCCTGGGTCAATCCTGGCTCCAACTGCTTTGCTATG GCT
WI-1304	124 T C ---	---	---	AAGTTTACAGAAAAAATACCAGAAAAGTGACTTCAAGANTCAGCTGAGATAGAAAACATATGCCCA TCATCTTCAANGTNOCCACAGACACTTATCCCTAGACAGCCATTTCTTTTGAATGN/T/CJGNCANT AAAAATGATTTGAAATTGGGAATAAGGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GGC
WI-1305d	202 C T ---	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATT/C/TJATGTTGGTAAATATAAAG ATTGTGCAAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46 C T ---	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAAT/CJTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153 T C ---	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202 C T ---	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

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WI-1306b	248 A G ---			TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAATCTTGTNGNNNTNG GGCTGGGTGACTGCGCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCCTJW/G/GC
WI-1306	240 A G ---			TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAATCTTGTNGNNNTNG GGCTGGGTGACTGCGCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTJAGTCTTCCCTAGC
WI-1307b	118 T C ---			GACAAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACTTTCTCTCACTTTCTCAAGTGGACA GATTTCTGCATTACTGCTGGGGTGGGGGAGCAGTGGTGTAGGCAATJ/CJGTGAGATTGCTTT CCTACCCCTCTAAATGTATCTTNC.TAATTAATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTGTGTGCTGTGTTTCTCCTGTAAAGNTGTTT
WI-1307	118 T C ---			GACAAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACTTTCTCTCACTTTCTCAAGTGGACA GATTTCTGCATTACTGCTGGGGTGGGGGAGCAGTGGTGTAGGCAATJ/CJGTGAGATTGCTTT CCTACCCCTCTAAATGTATCTTNC.TAATTAATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTGTGTGCTGTGTTTCTCCTGTAAAGNTGTTT
WI-1325b	169 T C ---			GAGAGATGGCCAAAGACAAGCAGAGGGAGAGAAAGCAACCNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCTTTGTCTCTTJ/CJACCCCTCAGAACTTCCCTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165 C T ---			GAGAGATGGCCAAAGACAAGCAGAGGGAGAGAAAGCAACCNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCTTTGTCTCTTJ/CJACCCCTCAGAACTTCCCTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162 T C ---			CTACGATAATTAGGTTGGCAGTGAGGGTATTAAGCTGTGTAGTGAAGAGTCCIGTTATTTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTGTGTJ/CJGAAGTTGGGTAGCTACCGGCCCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTCCATCTCTAAG
WI-1327	175 C G ---			CTACGATAATTAGGTTGGCAGTGAGGGTATTAAGCTGTGTAGTGAAGAGTCCIGTTATTTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTGTGTGAAGTTGGGTAGTJ/CJACCAGGCCCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTCCATCTCTAAG

WI-1341b	136 G A ---	---	TATCAGCATGATTGTGGCTGTGGACACAAAGTCAATTGTACTTTTGNIGCNNTCTTTCTTTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAAATTTGGCTTNCCTTTGTTNAATTATACCCAAAGC [G]A]GGATTGTGATGGATCTGTTATTTCTGTGCTTGGAACACGACAGTCGCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCCCAGCCACCTTGACCTTAGCAAGTGT
WI-1349e	192 G C ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]JTCAA ATAATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATA
WI-1349d	264 C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]JTCAA ATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATATGAT
WI-1349c	192 G C ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]JTCAA ATAATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATA
WI-1349b	264 C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]JTCAA ATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATATGAT
WI-1349	264 C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]JTCAA ATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATATGAT
WI-1403b	57 C T ---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/T]TCCGAAT GCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATTCTTGCCTGCATCATGCAITTTGGCAATATGTCACATAGCTGTCCCTCA TAATCCCAAAAGTGCCAAAAGGGTTGATCTGATTGT
WI-1403	58 T C ---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTGCTTCTCCGAA TGCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATTCTTGCCTGCATCATGCAITTTGGCAATATGTCACATAGCTGTCCCTC ATAATCCCAAAAGTGCCAAAAGGGTTGATCTGATTGT

WI-1417c	31 C T ---	---	---	CAGCGGGAAGAGATTACGTGGAGAGATGTC/TJTTGGCCAGGGCGGCAGATGTGAGCCACGGG GGTGACAGCATGCTGCTGGCAATTTGAGGGGCCAGAGAAATCCAGTGGCCCTCAATGACTTG GGTCTCTCGACTTCGGAAGTTTAAGGGCTCGGCTTCAAAAAGCTGGTCCGGTTTGAGGGGGTTGC AGCGAGGCCCTTAGGTCCTATTATGTTTGTGTAGAAAAAGTCGC
WI-1417b	31 C T ---	---	---	CAGCGGGAAGAGATTACGTGGAGAGATGTC/TJTTGGCCAGGGCGGCAGATGTGAGCCACGGG GGTGACAGCATGCTGCTGGCAATTTGAGGGGCCAGAGAAATCCAGTGGCCCTCAATGACTTG GGTCTCTCGACTTCGGAAGTTTAAGGGCTCGGCTTCAAAAAGCTGGTCCGGTTTGAGGGGGTTGC AGCGAGGCCCTTAGGTCCTATTATGTTTGTGTAGAAAAAGTCGC
WI-1729	172 A ---	---	---	CCATGAGCAACAGCATGTTCTACTCTGTGATGTGATGTTAGGGGCGCATGTATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATATGCAAAACATTTACAGGCAATGCGCTCGTAATAAAGA TGTTGGAGAACTGAAAAGAGAGCTTACATGCAACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGATGTGCTCTCCGTGGTNACCTTCTCTCCACCAATCACCCTGTGTTTTT
WI-1732b	122 T C ---	---	---	TGCCTTACTTCTTTGTTCAATCCACCATTACATTTTGTAAATTTGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAGGGGACATATTCAAGGAGTNTCCCTGGTCAACCCCTTTTCTAGTCT CTGCCACATGCTAGTAACGTGAGTGATGGTGCATCAGTATATCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATATTGGCTAAGGTATTTCATCATATTGGCTAAG
WI-1732	114 C T ---	---	---	TGCCTTACTTCTTTGTTCAATCCACCATTACATTTTGTAAATTTGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAGGGGACATATTCAAGGAGTNTCCCTGGTCAACCCCTTTTCTAGTCT CTGCCACATGCTAGTAACGTGAGTGATGGTGCATCAGTATATCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATATTGGCTAAGGTATTTCATCATATTGGCTAAG
WI-1750	97 A G ---	---	---	GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTTCCCCCAAAAAGGTTTTTAAATCTGTGTGGA CATAATGTTTGAATTTGCAGTTCACCTTGG/GJTTAAGGTGTGCTGTTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAAGGGCTAAGTCTTTGTAGTCAGACAAACCCGGCTTGCAGTCTGTGAG CTACATTCACCTTTATGATCTCCAGGAGGTTCTTCCA
WI-1780	31 A G ---	---	---	GGTACACAAGAAATGCTTCTGGAAATCTAC/GJTAGGGCCTTAACATTTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCAACCATGAAGCTGGCAAGAAACAATTCCTAGGAAAGTACAATTAC TGGAAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTTTCCCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAGAAATAATCATAAAAAT
WI-1803c	77 A G ---	---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTTCAGGCAGAA CCATTATGAT/GJAGTAGGGTAGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGTAAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATTACTTGTGCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAATACTGGAATCA

WI-1803b	77 A G ---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATATTTTCAGGCAGAA CCATTATGATGAGTAGGTAGAGCATCACACTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGCTCTCAA GGAATGGGAATACCTATAATACAGTCTATTGAGGAAAATACTGGGAATCA
WI-1837b	112 C T ---	---	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC[CT]CTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACTGGGAAGTCTGGGAACGTTTATAGCTTTCGTCTGGCT
WI-1837	112 C T ---	---	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC[CT]CTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACTGGGAAGTCTGGGAACGTTTATAGCTTTCGTCTGGCT
WI-1840b	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT[CT]GAGAACTCTGAATATTCAGCACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCCTAAAGAGCCCATGAAGAATTATAAGACT ATCGCA
WI-1840	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT[CT]GAGAACTCTGAATATTCAGCACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCCTAAAGAGCCCATGAAGAATTATAAGACT ATCGCA
WI-1879b	110 C T ---	---	GGGCTCACTTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTTGAGTNAAGGACCTGCCNTTTTAC[CT]GCTGCAAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGTTTAAATAGTCTTGTTGAATGAATTTCTGIGCGGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCCTTACCCACT
WI-1879	110 C T ---	---	GGGCTCACTTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTTGAGTNAAGGACCTGCCNTTTTAC[CT]GCTGCAAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGTTTAAATAGTCTTGTTGAATGAATTTCTGTCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCCTTACCCACT
WI-1900b	119 C T ---	---	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGCTGCATATGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTACAGCTGCAAAAGAGG[CT]GCTCTGAGAGGT AAAGTGCCTTCCCCAACCGGCACAACTAGAGAGCAGCCAAAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAAGTCCCATGAGAAACCACTTTTCTTTGCTCC



WI-1900	119 C T	---	---	TGTTCTCTGGTCCAGGACCGGGCTAAGTCTTGCTGCTAATGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTGCCTGCCCAACGCGCACAACTAGAGAGCAGCCAAACAGGTTTGAACCCAGCTCTGCCT GACTCAGATCTGTGCTTAAC TGCCATGAGAAACACATTTCTTTGCTCC
WI-1943c	165 C T	---	---	ATTCAGTTTACAGTGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165 C T	---	---	ATTCAGTTTACAGTGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164 C T	---	---	ATTCAGTTTACAGTGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1960c	270 A T	---	---	CCAGGTGAGGCTGAAAGAAGGAGGAGCAATTGCTGTGGAGTGGGATTCCTGGAGAAGCAACCT GCAGAGCTTCATTCTGTTTCAAAAGTGGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960b	270 A T	---	---	CCAGGTGAGGCTGAAAGAAGGAGGAGCAATTGCTGTGGAGTGGGATTCCTGGAGAAGCAACCT GCAGAGCTTCATTCTGTTTCAAAAGTGGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1977	203 T C	---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTCTTCATAGAGTNTTTTGTAGTCTCGTAATAATACTGTTGCCCTAGGAAGTTGTT TTTCTACTGCGTCTGTGAAAGCCTTTCCCATCGAGTGATACAGTACTTCCAGTTATGGAGATTIT /C/TAAACAATCAAACTGCTGAGGCTGTGG
WI-2012	102 T C	---	---	AAATTC TAGAAGCCAGAGTCAAGTCAAGTATTAAGTTGAAGTAAATGCA TTGTAGTTTCATGT TTTCTCTTAATCTGCACAAAACAGTAAAAATC/T/CJT TAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAAGCACTCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACITTTTTCTACTCTCAIT GGCTTACCATGCTTCCACTGGATC

WI-2013	127	C T ---	---	CTTTAGAGGTGGTCATTCGGTCCCTCTCGGAAGTGATTCGTGTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATAGTACACTC/TCTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTCAGTTATGCTCCCGGGTCC CCTTCACTGGAGGGATATCTCAGCTTCTGAGCCCTGGTTACTGCAATCC
WI-2032c	166	G A ---	---	ACCAGACATCCCATCAGGAGTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAACC ACATCACCCAACTGGTTTCTAGATGTACACG/AJGTGGGACCTCTGTCTCAACCTCCGACTTTTCAG AGATCATTGGTTAGGCTCACCTTCCGTGAATGCTTCTGTTTTCAAAAGGG
WI-2032b	219	C G ---	---	ACCAGACATCCCATCAGGAGTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAACC ACATCACCCAACTGGTTTCTAGATGTACACGTGTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTTGGTTAGGCTCA/C/GCTTCTCTGTAATGCTTCTGTTTTTCAAAAGGG
WI-2032	219	C G ---	---	CGTTTCTTCTACATCTTGGGNACATAAAGANGAAGAGNAGCTGCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTATGGTGGTTGGACAGCCAGGCTCAACAGAACTAATACCTGCTTC/C/TJCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGGAIGGGCTGCTTT
WI-2054b	188	C T ---	---	CGTTTCTTCTACATCTTGGGNACATAAAGANGAAGAGNAGCTGCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTATGGTGGTTGGACAGCCAGGCTCAACAGAACTAATACCTGCTTC/C/GTTCCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGGAIGGGCTGCTTT
WI-2054	183	T C ---	---	TGGGATTAACACCCCTGTTTCTTCTCCAGTTCAGTGTGCCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTTGCCGTTCAAAAGGTGTTCCGTGCTT/CJTGGA TATCATCTGATCTTCCCAACCCAGGCTTATTTATGCCCTAGGTAAAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573d	129	T C ---	---	TGGGATTAACACCCCTGTTTCTTCTCCAGTTCAGTGTGCCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTTGCCGTTCAAAAGGTGTTCCGTGCTTTCATAT CATCTGATCTTCCCAACCCAGGCTTATTTJAGCTGCTAGGTAAAGGGGTAAAGCAACAGAGGCTGTG TGAAGTGAATGATTTGCTTGACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165	A C ---	---	

WI-2573d	129 T C ---	---	TGGGATTAAACCCCTGTTTCTCTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTGCCGTTCAAGGGTGTTCGCGTCTT[C]TGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGACAAAGGTCATATGGCTGGCTTGGACGAG
WI-2573c	165 A C ---	---	TGGGATTAAACCCCTGTTTCTCTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTGCCGTTCAAGGGTGTTCGCGTCTT[C]TGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT TGAAGTGAATGATTTGCTTGACAAAGGTCATATGGCTGGCTTGGACGAG
WI-2573b	165 A C ---	---	TGGGATTAAACCCCTGTTTCTCTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTGCCGTTCAAGGGTGTTCGCGTCTT[C]TGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGACAAAGGTCATATGGCTGGCTTGGACGAG
WI-2573a	129 T C ---	---	GACTTCATGCTCATGAACAAGCATTTGCTCTTAATTTACAGACATTAAGAACAAGCTTTCC[A/G]CTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAACGCTTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2868b	60 A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTCTTAATTTACAGACATTAAGAACAAGCTTTCC[A/G]CTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAACGCTTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60 A G ---	---	CATGCTGTGTAACTCTGTGCTGTGCTGCGGGGAAATTAGAGCAAGGAATTGATATCTTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCATTTTAAATTAATACAGCTTTATGTCCACTTCTGTTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGCTTT
WI-2870b	131 T C ---	---	CATGCTGTGTAACTCTGTGCTGTGCTGCGGGGAAATTAGAGCAAGGAATTGATATCTTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCATTTTAAATTAATACAGCTTTATGTCCACTTCTGTTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGCTTT
WI-2870	131 T C ---	---	TGGGCTTTTACAAAGGAGGCTTT

WI-2954c	49 T A ---	---	---	TTAGCACATATCTGTTGGGACTTAACCTGAGACAAGGCATAAAAAATTAAGACACCTGGGGCA CAGAGGGAGCTCTATGCATTTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	---	TTAGCACATATCTGTTGGGACTTAACCTGAGACAAGGCATTAATAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	---	TTAGCACATATCTGTTGGGACTTAACCTGAGACAAGGCATTAATAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGAATTC/G CTGCCAGCACCATAAGCTTTCTTTCAAAACAATTTGTGTAACTCCTCCTCTTCTTAATAAACCTAAG ATTCTTTGTTCCCTGACATTCGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAGAAACCTTTTACTTAGGGATTGCT ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGAATTC/G CTGCCAGCACCATAAGCTTTCTTTCAAAACAATTTGTGTAACTCCTCCTCTTCTTAATAAACCTAAG ATTCTTTGTTCCCTGACATTCGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAGAAACCTTTTACTTAGGGATTGCT TTCTGGGAAAGAAAGATGGGGTTTTTTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTTAA /TAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT TTCTGGGAAAGAAAGATGGGGTTTTTTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTTAA AATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA AATGAGACAGAACTAGCAGAAAGTGTT TTCTGGGAAAGAAAGATGGGGTTTTTTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTTAA /TAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133 A T ---	---	---	TTAGCACATATCTGTTGGGACTTAACCTGAGACAAGGCATAAAAAATTAAGACACCTGGGGCA CAGAGGGAGCTCTATGCATTTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG

WI-2995c	151 G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA /TJAAATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151 G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151 G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA /TJAAATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133 A T ---	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCAC ATCTCACTTAGCTCCTT[C/T]CCTGCCATATCCTGTTTCTTACTCCTATCTCCTGAGACTTCTTCCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTINAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACITTTGCAAGG
WI-3147	85 C T ---	---	ATTCGTAAATGTTTTCACTGCTTCCAGTAAATTCITTTATGAGGTCCATGTCATTACCTCTACTTA[ T/C]GACAAGCAAGAAACAACAAGAAAGCCCTCTGTTTGAATCTGGCCTCTTATAAATACITTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAAATGGAATGTACTTATTTTATATCTTAT
WI-3234b	68 T C ---	---	ATTCGTAAATGTTTTCACTGCTTCCAGTAAATTCITTTATGAGGTCCATGTCATTACCTCTACTTA[ T/C]GACAAGCAAGAAACAACAAGAAAGCCCTCTGTTTGAATCTGGCCTCTTATAAATACITTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAAATGGAATGTACTTATTTTATATCTTAT
WI-3234	68 T C ---	---	

Accession	Position	Length	Sequence
WI-3292b	106	G A ---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTAGCTCTGCACTCATCC TCCCTGTCCCCGTCCTCCCAAGCCTATGTACTGGTATGCTGATGGTATGGATGGGATGGATTA GCGATGAATATTTCCATTGTTTCTCATTAATGATTAATTAAGTAAATATATTATTNCCATGA GACACAATGGAAAATGGAAAACATTTCATGGAAAAAACCCTTTCAATC
WI-3292	106	G A ---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTAGCTCTGCACTCATCC TCCCTGTCCCCGTCCTCCCAAGCCTATGTACTGGTATGCTGATGGTATGGATGGGATGGATTA GCGATGAATATTTCCATTGTTTCTCATTAATGATTAATTAAGTAAATATATTATTNCCATGA GACACAATGGAAAATGGAAAACATTTCATGGAAAAAACCCTTTCAATC
WI-3355	19	G C ---	CCATGAACCATGGGCTACA[G]CJATATTCTTAACCTCAGAGTCCCTCTTACTGGAGGGGATCCA CTTTTAAAAATATGATTTCTTGAAGTGGCTGCATCTATCTTCCCAAGCACCTTAAAACTCATCAGAA AAAAAATCATCAAAAAAGTCGAAGTTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3409	194	G A ---	CCATGAAGAATGAGTTTCTCTCCCTCCCTGGGTACGCTAAGAATAGCACACCCCTTGAGAAATTTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCCTCCGCTTAAGACACACCTTTATGCTTTCNAAAGCTTT CTGGAATTGGGATGAATCTNACATTCAATGTGCACCTTCGTGTGGGATCAGCTTCTCC[G]A]TGCCCC ATCTCTGNGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAAAATCAGG
WI-3505b	131	G A ---	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCTTGTATCATCAGTGCACCTTAAAAAATATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTAACACATTAACCTATTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAAATATGTTTGATAT
WI-3505	131	G A ---	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCTTGTATCATCAGTGCACCTTAAAAAATATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTAACACATTAACCTATTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAAATATGTTTGATAT
WI-3564b	177	C T ---	GCTAGTAAGGTTCCACCTAAATGGTTCCTCAAGTCAGGAGAGTCACATAATGTTTGGAAAAATAAAAGT GAAAAATCAATGTGTCTCCCAAGTGATTCACATGGCACAGTGTCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACCTGGTGAACCTAACCTAACATGCATGCTGTTC/TAACAAGTGTGTTGGGTGTCATC AGTGTACACATGCTACCTTCCCTTCACAAAAACA
WI-3564	177	C T ---	GCTAGTAAGGTTCCACCTAAATGGTTCCTCAAGTCAGGAGAGTCACATAATGTTTGGAAAAATAAAAGT GAAAAATCAATGTGTCTCCCAAGTGATTCACATGGCACAGTGTCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACCTGGTGAACCTAACCTAACATGCATGCTGTTC/TAACAAGTGTGTTGGGTGTCATC AGTGTACACATGCTACCTTCCCTTCACAAAAACA

WI-3649	64	A G ---	---	AATGTCATGCTGACTGACCTGTCTAACACACCTTTCCTAGTATCCCTTAGTGAAGATTACAG[G] AGACCAGTTTGCCTTCACTTAGTAGGGCCAATGATAGACTTTTTAGGTGCTACCACAAAGGTACCTGC ACAGCCACATCATATGTCACAGTATGGTTGCAAGGACCTGTCTAGACTCTTCTGCCTGCCTTGGTC TTCTGTTTTACCATAATTAATGATGACATGCAAAACCTCAGAGCCTTTTA
WI-3674b	133	G C ---	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCTCTCTAA ATTTAACTACCAGGGGAGTGCTTTTATAGTAATTAATAATGTTTATTAGAAAATAACAAAAT[G] /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAATGTAACTTGGTCAAAATGATTGT AATCTTAATTAATTGTTTTATGTTTTNATTACTGCCAATCACAGCCAAG
WI-3674	133	G C ---	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCTCTCTAA ATTTAACTACCAGGGGAGTGCTTTTATAGTAATTAATAATGTTTATTAGAAAATAACAAAAT[G] /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAATGTAACTTGGTCAAAATGATTGT AATCTTAATTAATTGTTTTATGTTTTNATTACTGCCAATCACAGCCAAG
WI-3682	137	G A ---	---	CAATATAGACCAATGACTGCCACAAGAGAAAATTAGTGATCTACATTTAGAAAACCCACATGTTTT ATTGGCTCTCTCTCTCTCTCTCTTTTAAATGCTCTCTCCAACACCAATTCACITTTATCTTTTCAA T[G/AJAGCATTTGTCCAATTTAAAGTCAATGAAAAAATAATGTACATTTTCAACAAGTATACATTAA GCCCTGCAAAAGTGCTTATGCTAT
WI-3854b	194	G A ---	---	GGTATGTTGAGGTACGCTAATGGTCACTGTGGTTTGGAGTGAATCTAAATGGATTTTTTGCCCTTGGGA CAAGACCAAGGACAACCTGATGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAAATCACTC TGGTTCAGGAAGGCAAGGGCAGTTATGACCACCTTTACAACCTGAGGAAATCAAAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-3854	194	G A ---	---	GGTATGTTGAGGTACGCTAATGGTCACTGTGGTTTGGAGTGAATCTAAATGGATTTTTTGCCCTTGGGA CAAGACCAAGGACAACCTGATGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAAATCACTC TGGTTCAGGAAGGCAAGGGCAGTTATGACCACCTTTACAACCTGAGGAAATCAAAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-4039	210	G A ---	---	AGCCAGCCACATCATGTTGAGTCTGCTCATCTTCCATCTCTATTTCTCTACTGCTTCAACCTT CCATTACAAGAACTCTTGTGATTACATTGATGTTTGGTTACACTACAGAATCCAAGATGACCTC CCCATCTCAAGGTCAACTAATTAACACCTTAATCTATTGCAATCTTTTGTCATTACCATTAACATATT CATGG[G/A]TTCTGGGATAAGGGGTAGACATTTTTATGGGAGGCATTA
WI-4110b	130	T C ---	---	GAAAAATGATGTTTTGATTTCCCTTCCCTATCTCAGATTATTGGAGTGCATTAGAAAACTGATAGT AACCCTTTTATTTGATGAAACTCTGCTCTATAATTAACCCCTCCTCTCTCTCTTTATTTTGCCCT[C]ACA GTTTAGGTAATAAAGATGCCCAAGAAATTCAGTATTCAGGTACAGTAAAAAGTAGCAACCAATGGG GTAGGCAAGTNCAGAAAAAGGAGGAGTNGGGGGTTTTCTGGGAAGA

WI-4110	130	T C ---	---	GAAAAATGATGTTTGGATTTCCTTCTATCTTCAGATTATTGGAGTGTCAATTAGAAAACTGATAGT AACCTTTTATTTGATGAAACTCTGCTATAATTAAACCTTCCTCTCTGCTTTATTTGGCCTTC/JACA GTTTAGGTAATAAAGATGCCAAGAAATTCAGTATTCAAGTACAGTAAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGAGGAGGTTGGGGGTTTCTGGGAAGA
WI-4119b	168	G A ---	---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAAATAG AATGGAAGGATAAATAAAGGTAACACGGGGAAGAACAGGACAAGACAGACAGAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTTCTTCA TGAGACCGTCTGCATTCTTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4119	168	G A ---	---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAAATAG AATGGAAGGATAAATAAAGGTAACACGGGGAAGAACAGGACAAGACAGACAGAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTTCTTCA TGAGACCGTCTGCATTCTTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4123b	51	T G ---	---	CAAAGTCAGATTTTGATTATTCAGGATAACAAATTTGAAAATAGAAAAGTG[T/G]TTAAACTATTT CAAATAACAATAAAGAAAACATGATGAAATTCCTCGTTACATAAATGATAGAAATTTAGTGGG TTCTCCATGACATTTGGCTTCTTCTCTCAACAGTGGTGGTGGATGTTTCCATGCTTTCTC AGGCACAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51	T G ---	---	CAAAGTCAGATTTTGATTATTCAGGATAACAAATTTGAAAATAGAAAAGTG[T/G]TTAAACTATTT CAAATAACAATAAAGAAAACATGATGAAATTCCTCGTTACATAAATGATAGAAATTTAGTGGG TTCTCCATGACATTTGGCTTCTTCTCTCAACAGTGGTGGTGGATGTTTCCATGCTTTCTC AGGCACAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145	G C ---	---	TTGTACATGTTTCATTCATCCCTCCCATCTTTTCTGTCTTAAAGAACCTCGCTTCTTCCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTTATTTCCATCAAGCTTCTCAGCATCTTCTATATACT GTGCTG[T/G]CCTTGGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTTGCITGAACGTGAGT AGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4149a	137	T C ---	---	TTGTACATGTTTCATTCATCCCTCCCATCTTTTCTGTCTTAAAGAACCTCGCTTCTTCCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTTATTTCCATCAAGCTTCTCAGCATCTTCTATATACT TTCGTGCTGTGCTTGGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTTGCITGAACGTGAGT TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4182	188	G A ---	---	TAACACACTTTTCATTTGGTTTCCCTATTACTGCAGTTAAAGGACCATCCATTATATTACAAATTCCTC AGTTCTATGCTTTAGAGTNCATTTATAGACTACTGTAAATTTTCAAGGGAATTTACTCCTTGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAAATTCAGGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCCCTTCCCAAGTTCTTAAATTCCTAG



WI-4230	93 T ---	---	AGAGACGTTGAATGGGGACATCTTTCTATTCGATTTTAGTTTAAACATTTGATAAGAAATGATGAAA GTTTGTCACATTCAGATTTATCTTTATAGCAGCAGAGCTGGCAAAATAAAGCAGCAGCTGACT TTTCCATGGTAAAGAAAGTTAGAGAAAACAGCCTATTTTCTTTAATGTTAAATGTAATTTCTGAAT ACATTTTAAATGGAGGAGAAATGAATAGTGACCTTTGAAATTTTGAATTTATGG
WI-4241	118 C T ---	---	GAAATTCCTATTGAAGTTTGGACCTTGAACCTGATCTCATTAATACTTTTNCCTGTAGTGGTTGTTT CATTTTGAACAACAGAACAGACGAAAAATTTCCACTTAAAAATTAATTTCTC[CT]AAGTATCTATGAT TTAGCACTGTTAGCACCAGAAACTGTGAAATTAATCTCTAGATATTTCTTCAGAACTAGGATGGAAG AA
WI-4271b	151 A ---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCAACCCCTCCCTTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A ---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCAACCCCTCCCTTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 G A ---	---	AATCGAAACATTGATTTTGTAAAGGAACCCACATTTATGATATTTTGCCCGAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAAGAAAGGATATTATGTCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4389	156 G A ---	---	AATCGMAACATTGATTTTGTAAAGGAACCCACATTTATGATATTTTGCCCGAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAAGAAAGGATATTATGTCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4488	31 A G ---	---	GATGACAAATTTATGTTGTTGGCATTTTAAAG[G]GTACCATTCATTTTCTTCTGGCTTTCTGTTGTT TGTTGTTGAGAAAGTCAGGGGTAGTCGTTAGTCCTTTTCTAGTTCTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAAATCAAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 G C ---	---	ACCATCAATGTATCACCTTCTAAAAATTTATTAGATGATTAACTGGCTCTGTTAAAAAATAAAACCT GTCTTGGACATTTGAAAAATAAACATTACTATTGTTGTCATTTTCTGCTACTACAAGGACTGACTA AACAAGTTAAG[G/C]GTTTGTGGAGGGGAAAAATCATAAAAATGCATAAAAAATTTCTACCACCTGTCA TTTCTTGTCCTCAATAAAATTTTACATGCGCT

WI-4584	144	A G ---	---	TTGGTTGGCATTAGCCTCATAACAACTATTACAATCATAATTGTTACTCTTATTACAAACAAG AAAAATGAGGCTTAACATCAGACTTCGTTAGTCGAGAGCCAGATTGAAACCCAGGAATCCATT CACCGTACAGTGCTACCTGGGTAAAAATGTTTAAATAAATCTATGGCATTAGATTTCAAAGA GTCCTAATGTGGTTTGAAATAGGTGTGCTTAATTGTTTATCAGTATGC
WI-4639	185	C T ---	---	TTTCTGCATTTGAATGTGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAAATCCACCAATTTAC TGACCATATGACTTGGGGAACATTATCTCACCTATCTGAGTCTGTATCC[C]CATCTTTAAATGTGA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA
WI-5327	63	A ---	---	AAATGAATCCGCTTTAGAGCAATACCAGTAAGGGCTGGTGAGGATGGTGGCTGAGAGA[A/- ]GATTACTCATAAAGCATATTAAATTTATAAATATGAAAAATTTAACTAGATAAATAAATGTGAAT TGAGTTGAAGGTGCATGAGAGTAGGAGGAGGAGGTCTTACTTATAGGGTTTATATAAGTNGCT TCAATAGAAATGGCTCTTTCCGGATGACAAATGATGAACGTCTTAAGCAGACAG
WI-5390	87	C T ---	---	GCTTTGAGAAATGAAAAGGGGAGCCTGGACCATTGAGGGCTTCTCACTCTGATTTTGTGTAT TTATTGTTACATTATTAT[C]TGCTGTCTCCCTTCTGGTATGCTTGTGTCATGAAACAATGAATTC CCCAGTGCCTGGCCGATTGCTGGCTCCTAGAGGTGTCAGAAAAAAGTTTCGGTGAATAGAAATTG ACGAATGGGTTCAGAAATGAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAGCAGT GCAACATTATTTTAAATTT[G/A]AAAGAAACTTGTTTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTTCCATGGTCGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTCAACAA
WI-5404	87	G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAGCAGT GCAACATTATTTTAAATTT[G/A]AAAGAAACTTGTTTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTTCCATGGTCGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTCAACAA
WI-5545b	77	A C ---	---	TAGGAAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATTCTTACCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA
WI-5545	77	A C ---	---	TAGGAAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATTCTTACCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA

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WI-5860b	134 A G ---	---	---	ACTCAAGTTTGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTTGTAAAGATTTTATTTGT TTCTTTTATATAAATTATGGATTTGTTTCTTCTTCCCTAACCAACCTTCTAACTGAGGAACACTAC[A/ G]TTTACTGGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-5860	134 A G ---	---	---	ACTCAAGTTTGGGGATAAAATCAGAAGTTTCTAIGTACAACCTTAAATTTTGTAAAGATTTTATTTGT TTCTTTTATATAAATTATGGATTTGTTTCTTCTTCCCTAACCAACCTTCTAACTGAGGAACACTAC[A/ G]TTTACTGGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-6106	208 C G ---	---	---	GCAACAACCTATTATACCTGATTCACACCCAGGTCTACTAACATTAATCAACCCTAACCAATAC TATATATTGCTCTGTTCTGAATTTATTTCAITTAGAATCTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTGTCTCCAGGAGTCTCAATGTGAAGTATAATCTTTACAGAG TAATTTC/GJATAGTAGGTCAACCAAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTGAGACTATAAGGAGATCAGGTGGAATAAACGAGGAAAAAACCTTC[C] AAACCTATATTNCTGCTTGTCATCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCTGAAATTTTATACCA
WI-6109c	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTGAGACTATAAGGAGATCAGGTGGAATAAACGAGGAAAAAACCTTAA ACCTATATTNCTGTC[C]TTGTGCATCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAAAATTATCCCTGAAATTTTATACCA
WI-6109b	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTGAGACTATAAGGAGATCAGGTGGAATAAACGAGGAAAAAACCTTC[C] AAACCTATATTNCTGCTTGTCATCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCTGAAATTTTATACCA
WI-6109a	129 T C ---	---	---	AATGCCTATCACCTTCCATCATGCTGCATAACTGATTGATTTCATAATGCTTATTTAGCACCTGTC TTCCAAACACATGCTGTTTGTTCATGATTC[C]GCATATCCCAAGTGCCTTAGACAAATGCCTCCCATAC AGTGAACAGTATTGACTAAACATACCTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC
WI-6112	96 T C ---	---	---	

WI-6244	103	T C ---	---	TAATTGCACAACCTACATATCAGGGTTTCTGATTGAAAGGAAGAGAATATCCCTTCTTTAGTGATT GCTTAATATTAAATCATAATAAGTGCACCATCTCTT/CJGCTCCTTATAAATGTTGTAGAAAGAGG AAATTGAGTGTGGGAATTAAAGCAACAGGAGACATTTTATATACTCCTACAGTGGGGAAGACTT CCTATTCTTTCCCAAGGATGGATACATTCTAC
WI-6268	124	C T ---	---	CTGGCCTTATAATCCAAAGTTTAGGATTAACTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTT GTCTACAAGATTTCCCTCCTAGTAGGGCTTTGGGTGTGGCACCGTTTGGCTCATTC/CJACTCTCCCT GGGTCTTATTGACTTTCAGGGAGCCTAGAAAGAGCTGGACAAAACCTGCTTCTTTGCAGAAAGAGTCG GGGTCCAAAGATTTCGTACGATTTTATA
WI-6336b	234	C T ---	---	AGGTGCCATTTAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATTCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCAGATGAAATGGACCATGTG GTACCCCAAGTGCATTATGTTCTGGTAGAGCC/CJTJGAGGACACTGACAGT
WI-6336	234	C T ---	---	AGGTGCCATTTAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATTCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCAGATGAAATGGACCATGTG GTACCCCAAGTGCATTATGTTCTGGTAGAGCC/CJTJGAGGACACTGACAGT
WI-6381	92	C A ---	---	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAATTA CAAAAATGNTTCATGTTTAAACA/CJAJGTTATTTAAAGCTCAACATTTTAAACAGGCACAAAT ATTCTAANGGCATATGCATTCACCATGGGCTTTTGAATGTCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTCAG
WI-6436	198	C G ---	---	GGTTGAGGCATTGGGAAAGGCAGAAATTTAGGCAGTAGAANAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAAAGTCATGACAGACAGGAAATACAAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGTGATAAATAAGAAGTTTAGACTTTGGTGGTTGAGTAGTTGTAGTAGTAGGTAGCGTT/CJ GJATTGGGTGATTCCACAGACAAGGTGATGTTCTAAGATTGATATTATTGT
WI-6449	186	C T ---	---	GAGGCCTTTTGGCTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTTCTGATTGGTTGGTGTGCTCAGACTGCCAGATTGTTAAATATTTTGAATAATC GTATCTGGTCTATTCACTGCAATCTCTGATCTTAIGCTGGCTATT/CJATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAAATTTTCIGGGTGATTTATA
WI-6449	186	C T ---	---	GAGGCCTTTTGGCTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTTCTGATTGGTTGGTGTGCTCAGACTGCCAGATTGTTAAATATTTTGAATAATC GTATCTGGTCTATTCACTGCAATCTCTGATCTTAIGCTGGCTATT/CJATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAAATTTTCIGGGTGATTTATA

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WI-6463	72 T C ---	---	GCTGGAGAGAAAGACCTCCAAAAGAGAAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACATTCJTGAAAAAAATTAAGTAGAACTCAAGAGAGCCAAAAAGTCCCAATTTGTGTCCATTA TAAGAAATATTTGAATGGAAATCTTAAGAAATGATTTTATTGATCAGTTAAATGTTCTTCCTCTCCTC CAGTCCCATTTATGACATCCGCATGCTG
WI-6474b	76 C T ---	---	AAGCAGTAAATCTTCCATCGCATGGATGCCAGTGGGTAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T ---	---	AAGCAGTAAATCTTCCATCGCATGGATGCCAGTGGGTAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A ---	---	GAACCTCAATTAACTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---	---	GAACCTCAATTAACTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---	---	CACATTTTGAATGCAACTGAGAAANTGGTTTNTAGGCTACCTTTTATTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATTCGTATCATTTTATAGNTCCCAAGCCCA TTAGCAATATCTTA[G/A]TCAAATTTTAAAGAGAGAACAGGAAATAAGGAAGGCCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACGTGTTCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTGTGTTGGTCTGTGTAAAG GTTCCTTGGCAGGAGAACATGCATATGACTTTAAAATAAAGACCAACA
WI-6564	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACGTGTTCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTGTGTTGGTCTGTGTAAAG GTTCCTTGGCAGGAGAACATGCATATGACTTTAAAATAAAGACCAACA

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WI-6608b	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGTC/- JAGTTGAGGAGCTAAAGGAGGGGATTCCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACTCCAGCACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCAGGCACTAGCTACAAGGCCACACCCAGAAAAAGGAA AGC
WI-6608	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGTC/- JAGTTGAGGAGCTAAAGGAGGGGATTCCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACTCCAGCACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCAGGCACTAGCTACAAGGCCACACCCAGAAAAAGGAA AGC
WI-6666	68 C	A	---	GTTAGACAGTATCCAGCAAAAAAGGTTATTTATACCTCTACTTTCCAAAAAGAGAAACCTCCCC A/C/AJAATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGCTTACTCTGTGGTTTCATGTAA ATGTTGGGTGACTCATTCGGCTCTCTNTCTCAAGTTCAGGCTTCTTGGGTAGACCA <sup>AA</sup> ACTA ATACACAATGTTAGAGCACACAAGAGA
WI-6670b	120 A	G	---	AGATTAAACATAATTATCTAGGGCCATTGTAGGGTNGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATACGTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/GJTTGTTAGCCA GCATTGCCATTCAGGCGCGAGTCAGGGTTTGTGGGCCAGAACTTTAGACAATTTGGGGAATCTGA AAAAAAGAAAAACAGAATTGTAAACACAGACACAGAACTTTAGAAGGGAT
WI-6670	120 A	G	---	AGATTAAACATAATTATCTAGGGCCATTGTAGGGTNGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATACGTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/GJTTGTTAGCCA GCATTGCCATTCAGGCGCGAGTCAGGGTTTGTGGGCCAGAACTTTAGACAATTTGGGGAATCTGA AAAAAAGAAAAACAGAATTGTAAACACAGACACAGAACTTTAGAAGGGAT
WI-6704c	33 T	C	---	TTTGAAAAATAAATTCATGCACCAATGTTTTAACT/C/CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T	C	---	TTTGAAAAATAAATTCATGCACCAATGTTTTAACT/C/CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T	C	---	TTTGAAAAATAAATTCATGCACCAATGTTTTAACT/C/CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106	GA	---	---	CCATGGACAGTTTAATTAGGAAGCTTCGACTTGTAGAATAACAGAGGAAGTCCAGTTATCTACCT ATTCCCTTAAACACACATTTTGTCAAGCTGGAATGATTCCC[G]ATAGTAAAACTCAACATCCACACCT GCATAAACATCGCCTCCCAAGTGACTATTATTAAGTGTGACACAGGATGTCACCAGTGAGCCTC ATCTCCAGTCCAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148	GC	---	---	AAAACAAATGGTGCAATTCGATAATATTGGGTACACAGTATAAAACATAACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTTCTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGAGGNGAACTTACCCAAATCCAGTCCCTTCTTC
WI-6766	148	GC	---	---	AAAACAAATGGTGCAATTCGATAATATTGGGTACACAGTATAAAACATAACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTTCTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGAGGNGAACTTACCCAAATCCAGTCCCTTCTTC
WI-6787b	97	A	GC	---	ACAGATAAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACCTTGTGCAGCAATGTTCAAATTTTACAGTCTTCTTGTCTACGAAATNCTGCAGATCCTTATGT ATGCTTTGTCTTCTTGGGAAGGACGGTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTGCATAGGGCAGAGTAGANTACTCACAGGAAAGAGTAAATTCAGGT
WI-6793	105	C	GC	---	GAACCCACAGGTCCTGTTATTTTAAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGCGGCTTCAAATCAATCAGTCAACCCCTC[G/G]AGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTTGGCTGTAGGAAGTAGGGTTAATGCCCTCTAATCCCGGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAAGTTTCTATCAGAGTAAAGGCAAC
WI-6810b	37	T	C	---	CACAATAATAAATCACTCCCTACCTGAAACCTTTAT[C/J]AGAAGCATTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTGTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCTTTTAAATGCTATGNACAAGTACAATTTCTTTTGTAGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6810	37	T	C	---	CACAATAATAAATCACTCCCTACCTGAAACCTTTAT[C/J]AGAAGCATTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTGTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCTTTTAAATGCTATGNACAAGTACAATTTCTTTTGTAGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145	C	A	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTTCTAGTA TTTGTCTTTTGTATCCAGTTAAGACCATCAGCATATACACATCACTCACTCAACAATGTAGCT GCAGGTAAC[C/J]ATGTGGATACCTGTGTCTCTACTNGCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAATCTTGGTTCAGGTGGGCTGTGCAG

WI-6817	145	C A ---	---	GCATGATTAACCCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGCAGGTAAC[C]/AJGTGGATACCCTGTGTCTACTNGCCTCCAAAGGCATTCAGGGATCATCA AAGATGTTGGACACCCTGTGTTCAAATCTTGTTTCAGGTGCGGCTGTGCAG
WI-6813b	221	C ---	---	GATGAAAGCCATTTATTTTCTCTAAATTTTAAATAGAAGACTTAAATGGAAAAACATTTAGTACCATGTGACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCTAGTAAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAAATTTCTGCTATTTTGCTTTAGCAACAGCAATAACTTTTGTTTCCTATATGACACCTAATATCCAG
WI-6819a	175	G T ---	---	GATGAAAGCCATTTATTTTCTCTAAATTTTAAATAGAAGACTTAAATGGAAAAACATTTAGTACCATGTGACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCTAGTAAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTT[G]/CATATACAAAAATTTCTGCTATTTGCTTTAGCAACAGCAATAACTTTTGTTTCCTATATGACACCTAATAT
WI-6826b	154	A G ---	---	GCAAAAAGCTTTATTGGCTCCAAACAAATTAATCCCTTTTAAAACTCCTCTCTCTCTGCTCAGTGGAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[G]/GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACGTGTAAGCTGAATTGCAAAATATGGCAACACACACTGGAGCTGGGGTATACGTTG
WI-6826	154	A G ---	---	GCAAAAAGCTTTATTGGCTCCAAACAAATTAATCCCTTTTAAAACTCCTCTCTCTCTGCTCAGTGGAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[G]/GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACGTGTAAGCTGAATTGCAAAATATGGCAACACACACTGGAGCTGGGGTATACGTTG
WI-6857a	122	T C ---	---	AGTGCAAACTATTTGAACAAAAGTAAACTATGAGTCACAGCATTCAGACATCAGACACACGGGAAGTGGAACAATAATTCACTAAGTAAATACAGCAGATGAGATGCTCTCACATGTAT[C]/ATTTAATATTCATGCTTTTCAATAGTCTCTTAGTCAACTTCAGTGAATTTCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAAGTTTGGCAACTGT TGGGGCTAATT
WI-6865	153	G A ---	---	TTATAGAATACTTATGGGGCATACGNGTAAATGAACCTGCAACCTTAAAACTTAAACAAACAGCTTGTTGTGGTTCGCTGAAATCCTCCCTGCTCACAACACAGCAGCTACTNGGTTTCTTAAAAAGACGTATTTGCAGGCAAACTTC[G]/ATAGAGCCATTCGTGCAGAAGAAGGGAAGGAGCTGTTGTTTACCTGTAGTGAAGATATCTTTGCGCTGTTAGAACTGAGCTCATTA
WI-6899	73	C T ---	---	ATTGAAAACCTGGTAGCAACAGATAAATTACAATAGAGCCTGGATATAAAAAAGAGAGAAGATGCAGACTT[C]/AAGCTTATAGAGAAAGTCAAAAAGGAGCAAGTTTTTGAATCAGATTTTATGATACGGAAAAAAATTTCCCTTTTGGCAACAGGATTATTCGAAATAATAAATCTGCCAGTGCCCAATCAG AAACACCAATTCACAATAATTTGCATGCCCCCTAGTGGCTATTTTATACATACT



WI-691 <sup>nb</sup>	163 G T ---	---	---	CACTCAAAACCTTTTATTCATTGATTACAAACTGTACAATATTTACAAAGTTTAGGCATTATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAAATAAATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACITTAAGCCATTACCAATAGTGTGAGATGAATGGAGAAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCCGGACCTTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144 A ---	---	---	GCTTGTTTTTTTGTGTTTTTAAAGTGACACCTTGGCCCTTGTGGCAATTCCTCATTATCTTACCC AAAAGTGCCTTTGGGCCAGCCACTGACTGATTTAAACCCAGAAATGTGGTTTTAAACAATGTGGT CGTGTGAATTCAGGTGATTTTATTTCTATTTGGTAGTATTTTCAGATTTTCCACAAAGAACATG TATTGCTTTGTAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175 T C ---	---	---	CAATCAAAAAGTTCAGATTTCAAAGCTGGGATGAAAGCCAGGCTCTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACCTCTTAATTTTCATGTCCCAG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCACTAAAGGTTC/AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175 T C ---	---	---	CAATCAAAAAGTTCAGATTTCAAAGCTGGGATGAAAGCCAGGCTCTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACCTCTTAATTTTCATGTCCCAG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCACTAAAGGTTC/AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79 G A ---	---	---	TTTTATGAACATTTTCAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCTAGGTAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAAACTATAGGTAGTATATTAAACAAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6955	79 G A ---	---	---	TTTTATGAACATTTTCAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCTAGGTAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAAACTATAGGTAGTATATTAAACAAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6957	47 C G ---	---	---	AAACTAAAACCCCTTATTGTCTCCAAGTGTGGCAAAATAGAAAAT[C/G]TTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATTCACCTTAAGAGCATTCAGTCAAAATATACAAAA ACAAATTCAGATTGCTTGGATCTTGGTCATTTATGGCTTGAAGAACTGGATTTGAAAAACCACTTTAGG CTAAAATAAATGATATGAATAATGATAGACTGTGATCTAGAAAAATCATGC
WI-6996c	242 G T ---	---	---	ACTCTAGTGCCTCTGTACCACCACTCTAATGCCCTCTGGTGGCCGACCTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGTCTCAGCACCCAGAGGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTTCC[G/T]GTGGGATC

WI-6996b	242	G T	---	ACTTCTAGTGCCTCTGTTACCAACACCTCTAATGCCTCTGTGGCGGCACCTCTGATGTCGGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGCTTCAGCACCCAGAGGAGGAGAGCGCGCAGTTCCTG CAGGAGAGAGGGGGCTGCTGGACCCCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCTGATGGTGGGCCCTCTGTGCTCTCTCTTCQ[G]TTCGGATC
WI-6996	228	T G	---	ACTTCTAGTGCCTCTGTTACCAACACCTCTAATGCCTCTGGTGGCGGCACCTCTGATGTCGGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGCTTCAGCACCCAGAGGAGGAGAGCGCGCAGTTCCTG CAGGAGAGAGGGGGCTGCTGGACCCCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCTGATGGTGGGCCCTCTGTGCTCTCTCTTCGGTCCGATC
WI-7021b	112	G A	---	TGGGAGGACAGGGAGATGCTGCAGTTCACAAAGAGAAGGTTCTTCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTGAAAGCCACAGACAATATGGTCCCAAATG[A]CCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTTCGGTTCACATCCACACAGCCAATCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G	---	TGGGAGGACAGGGAGATGCTGCAGTTCACAAAGAGAAGGTTCTTCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTGAAAGCCACAGACAATATGGTCCQ[A]GATGCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTTCGGTTCACATCCACACAGCCAATCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T	---	GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGAGAGCCTGCATCCCAGGATGCGGGTGG CCCTGCAGCCTCCTCCACCTCACCCTCCATGACAGCGCTAAACGTTGGTGA[C]TGGTGGGAGCCTCT GGGCTGTTGAAGTCACCTGTGTGTTCCAAAGTTCCAAACAACAGAAAGTCATTCTCTTTTAA ATGGTCTTAAGTTCACAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7056b	118	C T	---	GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGAGAGCCTGCATCCCAGGATGCGGGTGG CCCTGCAGCCTCCTCCACCTCACCCTCCATGACAGCGCTAAACGTTGGTGA[C]TGGTGGGAGCCTCT GGGCTGTTGAAGTCACCTGTGTGTTCCAAAGTTCCAAACAACAGAAAGTCATTCTCTTTTAA ATGGTCTTAAGTTCACAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7091b	153	A C	---	AATTGCTGAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAAAGGCATATGGAGAACATGTTTATCTGCTCTATAAATAGTATCCAATCACTGTG CTTAATTTAAATAGCATT[A]CTTATCATTATCAGCCTTTTATGATTTTCCAAAGTAAATATTA ACATATTATTCATTGGTCTCTCTTTTATCTGTTCTATATGAATGCTAT
WI-7091	153	A C	---	AATTGCTGAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAAAGGCATATGGAGAACATGTTTATCTGCTCTATAAATAGTATCCAATCACTGTG CTTAATTTAAATAGCATT[A]CTTATCATTATCAGCCTTTTATGATTTTCCAAAGTAAATATTA ACATATTATTCATTGGTCTCTCTTTTATCTGTTCTATATGAATGCTAT

WI-7136	58 T C ---				TGTGAAGCCACATTTTCCAACATGAGCCTCATGAAGCCAACTAAGTGTATTGAACGTGTC/JAATTC TCTCAATAACTCAGTGTAGCACITTTAAAGTCTGAAGGACAGCAACATGAAGAGGACATATCAATGTG GTGGAGAAAGGGAAGGGTGGCTTTTAAATTTATTTTCTTCATCTTTTATAACAAAGAAAGNNNNN NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTAGCTTCTATATATG
WI-7146c	210 A G ---				GGGACGCCTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTTCCATTTCGTTTAGCTG AATAATGAGTTGTTCTTAGAGGAGACAGCCTGTCTCTCTTGTGCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTGTGGCCCTCTCTCGCATGCC AACGC/JG/GTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146b	210 A G ---				GGGACGCCTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTTCCATTTCGTTTAGCTG AATAATGAGTTGTTCTTAGAGGAGACAGCCTGTCTCTCTTGTGCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTGTGGCCCTCTCTCGCATGCC AACGC/JG/GTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146	202 G A ---				GGGACGCCTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTTCCATTTCGTTTAGCTG AATAATGAGTTGTTCTTAGAGGAGACAGCCTGTCTCTCTTGTGCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTGTGGCCCTCTCTCGCATG/A JCCAACGCAGTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7153	161 A T ---				ATATTACAACTTGCTTTTAGCTGATCTCCATCCTCAAAATGACTCTTTTCTTTTATATGTTAACATA TATAAATGGCAACTGATAGTCAATTTGATTTTATTAGGAACATCTGAAATCTGCTCAGAGCCT ATGTGCATAGATGAACNNNNNNN/JA/AAAAAAGTTATTAACAGTAATCTATTACTAATTAT AGTACCTATCTTTAAAGTATAGTACATTTACATATGTAAATGGTATGTTT
WI-7155	156 T G ---				TAGAATAGATGCGGTCATATTTCTTTGGCTTCTGGTCTCCAGCCCTCATGGTTGGCATCACATAT GCCTGCATGCCATTAAACACAGCTGGCCCTACCCCTATAATGATCCTGTCTCTAAATTAATACAC CAGTGGTTCCTCCTCCTGT/JG/JTAAAGACTAATGCTCAGATGCTGTTACGGATATTTATTTCTAG TCTCACTCTCTTGTCGCCAGCCTTCTCTCTTCCCCATTCCCCAAGTCCAG
WI-7169b	161 A G ---				AGCTCCACCAGATGCAGATTGTGTTTGTGTTTCTTGTATCAGTGTACACAGCTTATAACATGTAT GCTTTTCAGAAATACAGTTGCTAGCCAAGCCCATCAAGTGTCTGAAATCAATATTGGTTTATGCAAT ACAGCAAACTTTTATTAGTAGAT/JG/JGAGAGAAATGTTTAAATATTAGGAATCCTAGACCATA TTTTCAAGTCATCTTAGCAGCTAGGATCTCAAAATGGAAGTGTATATATA
WI-7175b	194 C T ---				CTCCTAGACTAGTCTTTACCTTTTATTAAATGAAGTGTGACAGGAAGCCCAAGGAGTGTCTCTCACCA ATAACTTCAGAGAAAGTCAGTTGGAGAAAAATGAAGAAAAAGGCTGGCTGAAAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAAATATATAATGGTTTACTGCTGTCATTGTCCTATGCCTA/C/TJAGAT AATTTATTTGATTTTGAATAAAAAACAATTTGTACATTCCTGATACTGGG

WI-7175	194 C T ---	---	---	CTCCTAGACTAGTGTCTTACCTTTATTATGAAGTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCA ATAACTTCAGAGAAAGTCAGTTGGAGAAAATGAAGAAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGCTGTCAATTGTCCATGCCTA[C/T]JAGAT AATTTATTTTGATTTTGAATAAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273 G A ---	---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCCCTGAGCCCAAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTCCTAGGGGAACAGACCAAGTGAACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTCTGCACCTAAGAGAAAATTCGCACTAATGAATCTCGTTCCCAAGAACTACCC ATCCAGGGCTGGCTCTGCACCTAAGAGAAAATTCGCACTAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7178	273 G A ---	---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCCCTGAGCCCAAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTCCTAGGGGAACAGACCAAGTGAACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTCTGCACCTAAGAGAAAATTCGCACTAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7182b	116 A C ---	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGTGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCCTCTGCAACCCACTCTGAGCCTTACCTCTCTCTCTCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTTCAGCTCAAGAGATGCCCTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAAATGGCAGCTATTTCCTGAAGCCTAGTACCCCAATT
WI-7182	106 C A ---	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGTGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCCTCTGCAACCCACTCTGAGCCTTACCTCTCTCTCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTTCAGCTCAAGAGATGCCCTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAAATGGCAGCTATTTCCTGAAGCCTAGTACCCCAATT
WI-7191b	273 T A ---	---	---	ATAATTGCTTGTCTAGCCTGGCAAGATATTTTCATAAAGAGGGGATAACAATGCTGATTACTAC CTTTTAAATATTTTAGATAAATGCACAGCACACACACACATCTAAGCATTTAGTGATGGTAGC TGATGTCAGCTTCATGTGGAATTTAAGCAGCTCTAGAAACAATGAAGCTTCTGGCATAATTTAAGGAG CTCCCAAAATGTGTTACCTATTAAATGTAACCTAGCAAGTAGAAGACCAATT
WI-7199c	112 T C ---	---	---	CCCAGTGTGAACAGAACCTCCCAAAATTTGAGTTGCACCCCTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT/CJGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTGTGGTCTCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCCTCAGTTCCTCACCACATCATCTGTCTAA
WI-7199b	112 T C ---	---	---	CCCAGTGTGAACAGAACCTCCCAAAATTTGAGTTGCACCCCTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT/CJGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTGTGGTCTCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCCTCAGTTCCTCACCACATCATCTGTCTAA

WI-7216c	237	T C ---	---		TGACACTAACACCTCTAAITCAAGCGAATGTTGGAACACCATGAACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTCTGTATACATAGGAAAAGACACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCCTCTGAGGCTAAACACAGTTTGTCTTTCCTGTAATCAGTT
WI-7216b	237	T C ---	---		TGACACTAACACTCTAAITCAAGCGAATGTTGGAACACCATGAACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTCTGTATACATAGGAAAAGACACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCCTCTGAGGCTAAACACAGTTTGTCTTTCCTGTAATCAGTT
WI-7220b	147	A T ---	---		AGGATGATGCTCCAAAAGGGACCTTGAACCTATTCAACCATTTTGCTCTTTAAGCTGGCAACCCCA TCATTAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCAGTAGAAATJAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7220	140	A T ---	---		AGGATGATGCTCCAAAAGGGACCTTGAACCTATTCAACCATTTTGCTCTTTAAGCTGGCAACCCCA TCATTAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCAGTAGAAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7226	232	C ---	---		GATCGAATTTTTCAGATGATCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATGTATA TACATATCAGCTCTTATCTCTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTGTGATCATTT CCCTTTCCATATAGGAAACATAATTTGAAAGTGGCCAGATGAGTTTATCATGTGCAGTGAAAAATAA TTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACCTCTTGGGGTTT
WI-7228b	254	G A ---	---		ATAGCTCCAGATTACAAAGGGCAAGGTAATAGAAATGCATACCAGTAATGGCTCCAATTCATAA TATGTTCAACGAGGATTACAAATTTTGTCTCTTCTGTCTTTGTAACTATTTAGTTGATTTTAATTA CTTCTGAATAACGGAAGGATCAGAAATATCTTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTTAAAATAAGAAATGTTATCCAACCTATTAAGATATCTCAATGTT
WI-7228a	163	G A ---	---		ATAGCTCCAGATTACAAAGGGCAAGGTAATAGAAATGCATACCAGTAATGGCTCCAATTCATAA TATGTTCAACGAGGATTACAAATTTTGTCTCTTCTGTCTTTGTAACTATTTAGTTGATTTTAATTA CTTCTGAATAACGGAAGGATCAGAAATGTTATCCAACCTATTAAGATATCTCAATGTT
WI-7233c	213	C T ---	---		CGATCGTACTGCCAGTAGCATTTGTCTGTCTGCCGCTTGTGTTGTACATTCATTTCAATTTGTACA GATGTGAACCTTTATTCCTTGTCACTAATTAATTTAAATATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTCTGCCACCTTTTGTGGCAATATTAAAGTGAACCTGCTAATA GTGTAAGTATCTGTGCACAAAACCACTGCCAGATAACCAAGAGGGGCTG



WI-7252a	520	T C ---	---	CCACAGGATCCAGCCAGCGGCCCTCCGCCCTCCCACTCGCAGCAGCGCGGGGACAGAG GCCTGCCCGGGCGCGCAGCCCGGCTGGCTGGAGGCTGCCCCGGCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCGCAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAATCAGTCATTAGACTCCTCCTCCA
WI-7265m	252	T A ---	---	AAC TTGGTTATGTCAGTTCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCAACCATTCCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCTT
WI-7265l	231	T A ---	---	AAC TTGGTTATGTCAGTTCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCAACCATTCCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265k	121	T G ---	---	AAC TTGGTTATGTCAGTTCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCAACCATTCCTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265j	174	T A ---	---	AAC TTGGTTATGTCAGTTCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCAACCATTCCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265i	227	T C ---	---	AAC TTGGTTATGTCAGTTCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCAACCATTCCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265h	80	T A ---	---	AAC TTGGTTATGTCAGTTCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCAACCATTCCTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265g	170	T G ---	---	AAC TTGGTTATGTCAGTTCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCAACCATTCCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT

WI-7265f	231 T A ---	---	AAC TTGGTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCCATTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGATAGTATTTGTTTATATATATGTAATAAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTT/AJ/AAGGAGTAAAGATTGGCT
WI-7265e	227 T C ---	---	AAC TTGGTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCCATTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGATAGTATTTGTTTATATATGTAATAAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGGCT
WI-7265d	174 T A ---	---	AAC TTGGTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCCATTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGATAGTATTTGTTTATATATGTAATAAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265c	170 T G ---	---	AAC TTGGTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCCATTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGATAGTATTTGTTTATATATGTAATAAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265b	121 T G ---	---	AAC TTGGTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCCATTCTGTGTTTCATTGTAGTT GTTAAGGAAACCAAGCATATAGATGATAGTATTTGTTTATATGTAATAAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265a	80 T A ---	---	AAC TTGGTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTT/AJTATTTGCCACCAAAAAGTAAATGCATTTTCCACCCATTCTGTGTTTCATTGTAGTT GTTAAGGAAACCAAGCATATAGATGATAGTATTTGTTTATATGTAATAAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7281b	183 C ---	---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCCAAGC ATCTCCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTTGGCAAAAACGAGTCCGAGGCCGCGAG GTGTTGTGAAGACCACTCGTCTGTGTTGGGTCTTCAAGAGGCCCTCCTC
WI-7281	171 C A ---	---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCCAAGC ATCTCCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTCAGACTCTC/AJTGGCAAAAACGAGTCCGAGGCCG CAGGTGTTGTGAAGACCACTCGTCTGTGTTGGGTCTTCAAGAGGCCCT



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WI-7301	205	A C ---	---	---	AACTATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGGAGGATATGATGGTTACAAATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAAACAGCAATCA AATTTCATGGACACATGAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7314c	49	G A ---	---	---	CTCTCTTTTCTTCAGATCTGCTCCTGGTAAATTTGGAGGTCA[GA]TTGTTCTACCTCACTG AGAGGAACAGAGGATATTGCTTCTTTGCAGCAGTGAATAAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTAGTCTACCTTTATTTTATTAAACAAACTTGTTTTT
WI-7314b	49	G A ---	---	---	CTCTCTTTTCTTCAGATCTGCTCCTGGTAAATTTGGAGGTCA[GA]TTGTTCTACCTCACTG AGAGGAACAGAGGATATTGCTTCTTTGCAGCAGTGAATAAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTAGTCTACCTTTATTTTATTAAACAAACTTGTTTTT
WI-7314	36	A G ---	---	---	CTCTCTTTTCTTCAGATCTGCTCCTGGTAAATTTGGAGGTCA[GA]TTGTTCTACCTCACTG AGAGGAACAGAGGATATTGCTTCTTTGCAGCAGTGAATAAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTAGTCTACCTTTATTTTATTAAACAAACTTGTTTTT
WI-7321b	199	C T ---	---	---	ACTCAGGGAAGGATGCCCCATTAAAGTGACAAAGGGTGGGTGGGCACCATTGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGACTGCTTTGGCATCCAGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNNAGGTGGCACACCCCATC[C TTGTTGCTGGGTGTGGCAGCCACATCCAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199	C T ---	---	---	AGACATCTCGCTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGACCCACGAAACTGCCCTGGC TCCAGTGAACCTGGGCACATGCTCAGGCTACTATAGGTCCAGAACTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATAAAATCTGAATTTTGGGATTTTCAAAAGATAATATTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGCGAGCAACCTATAAATCA[AC]CA
WI-7336b	248	A C ---	---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGCAGAGAACAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTCTCTTTACACAC[AG]TATACACACAGACATCAGAAATTCGTGT
WI-7338c	221	A G ---	---	---	

WI-7338b	125 A C ---	---	CTCTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAAAGAAACAGCAATCAATATATAAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACACAGACATCAGAAAATCTGTT
WI-7338	125 A C ---	---	CTCTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAAGAAACAGCAATCAATATATAAAATTCAAAGACTATCTGCAGCTA GTGTTTCTCTTTACACAC[A/G]TATACACACAGACATCAGAAAATCTGTT
WI-7384c	146 T A ---	---	CCTATGTCATGAATGCTAGGGGCCAGGGAACAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAATAACTTTAAAAATACCATTAAATACATTTGATTTTCATTGTGAACAGGTAATCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384b	146 T A ---	---	CCTATGTCATGAATGCTAGGGGCCAGGGAACAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAATAACTTTAAAAATACCATTAAATACATTTGATTTTCATTGTGAACAGGTAATCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384	145 T A ---	---	CCTATGTCATGAATGCTAGGGGCCAGGGAACAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAATAACTTTAAAAATACCATTAAATACATTTGATTTTCATTGTGAACAGGTAATCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7388c	106 A T ---	---	TGAAATCCTGGTCTCTGGCCTGCTGAGCTGGTTATTTTACTTTGCCCTCCCTCCCTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACT[A/T]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTACCCTCTATTTGCCACAAGCGTCTCGGGATTGTTTGA CTTGTGCTGTCCAAAGACTTTCCCCCAAAGATGTTATGTTATG
WI-7388b	106 A T ---	---	TGAAATCCTGGTCTCTGGCCTGCTGAGCTGGTTATTTTACTTTGCCCTCCCTCCCTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACT[A/T]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTACCCTCTATTTGCCACAAGCGTCTCGGGATTGTTTGA CTTGTGCTGTCCAAAGACTTTCCCCCAAAGATGTTATGTTATG

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WI-7388	94	T A ---	---		TGAAATCTGGGTCTCTGGCCCTGTCCTGTAGCTGGTTATTTTACTTTGCCCCCTCCCCACITTTTT TGAGATCCATCCTTTATCAAGAAAGT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTTGCCACAAGCGTCTCGGGATTGTTTGA CTTGCTGCTGCTCAAGAACCTTTTCCCCCAAGATGIGTATAGTTATTGG
WI-7438	64	A G ---	---		TTAGATTTTAAATTGGCAACCAGCAACTCACTGCCACCATTCCACTGCAGATCINCTATTCCTGG[A/G] GTTGATATGACAAGGAAACCTTATTGGAACCAAGTCTTCAGATTGTCAGATGTCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTTCACTGTAACATAGTTTGCTGCTGTTGTTA TTGAAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152	T C ---	---		CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAAACTGAGAAATGAGAAACCTTGATAGCACTGTCTGAATGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGCTACTTCTCAAAATGTTTTTGACA
WI-7454	152	T C ---	---		CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAAACTGAGAAATGAGAAACCTTGATAGCACTGTCTGAATGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGCTACTTCTCAAAATGTTTTTGACA
WI-7464c	177	G C ---	---		AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAAAATGACACTTATTCCAAATAAAATTAATGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCACTAAATCTATTATAATTCCTATGTA CAACAGAGCCACAGCACAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAAGCAACGTTCAACCAAAATTAT
WI-7464b	168	C A ---	---		AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAAAATGACACTTATTCCAAATAAAATTAATGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCACTAAATCTATTATAATTCCTATGTA CAACAGAGCCACAGCACAGAGGGTGGGCATAAGCAGTTGCCAAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAAGCAACGTTCAACCAAAATTAT
WI-7464a	103	C A ---	---		AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAAAATGACACTTATTCCAAATAAAATTAATGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCACTAAATCTATTATAATTCCTAT GTACAACAGAGCCACAGCACAGAGGGTGGGCATAAGCAGTTGCCAGGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAAGCAACGTTCAACCAAAATTAT
WI-7499b	134	T G ---	---		CAATTTCTCAATCCAACTAGTGTGTTGCTTAAACCATTCAGACAACTCCACATTCGAAGGTTTTTA AATGCAATAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGTTCTTTGAATGCTTCAIT /GJTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTAGGA ACTCTGTACAAAATCCCTTTGAAAATATAAATTTTGGAAATGAGTGATGA

WI-7499a	33 A G ---	---	---	CAATTCTCAATCCAACCTAGTCTGNTGCTAA[A/G]CCATTCCAGACAAACCTCCACCTTCCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTGAATGCTTC ATTATAGTCTCTTCATTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTITTAGGAA CTCTGTACAAAATCCCTTTGAAAATATAAAATTTGGAAATGAGTGATGA
WI-7506b	118 A C ---	---	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCCAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGAGTAGTCTGTGCTGATTGCCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGAAATGAGTGAAGAGGAAAAATCATGATGTCATGATGCAGTAATTAATGATGCA GAAGAAAATATTTAAATAATTGGACCACCTTGTTCTACCATCCCTACCCACT
WI-7506	118 A C ---	---	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCCAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGAGTAGTCTGTGCTGATTGCCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGAAATGAGTGAAGAGGAAAAATCATGATGTCATGATGCAGTAATTAATGATGCA GAAGAAAATATTTAAATAATTGGACCACCTTGTTCTACCATCCCTACCCACT
WI-7534b	143 C T ---	---	---	TGTGAATTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGTTCTTGATGTTTCGCAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATTCGCCGTGATAGAAATTGCT AAATTGTCGTGAAATAGGTTAGAAATTTCTTTAAATATGTTTTCTATTTCGTGAAAAATTCGG AGAGTGTCTGCTAAATTTGGATTGGTGGTATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C ---	---	---	TGTGAATTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGTTCTTGATGTTTCGCAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATTCGCCGTGATAGAAATTGCT /C/JAAATTTGTCGTGAAATAGGTTAGAAATTTCTTTAAATATGTTTTCTATTTCGTGAAAAATTCGG AGAGTGTCTGCTAAATTTGGATTGGTGGTATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ---	---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCTGTTTGACAGGGAAGCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTCTTTCCTCTT[A/G]GGAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7543	162 G A ---	---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCTGTTTGACAGGGAAGCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTCTTTCCTCTT[A/G]GGAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7555c	60 T C ---	---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATTCCCTCAAAATTTGTAGAGGTCTCTTA AAAAAGAGTGGTATGTTGTGATGATGATCAGCACTAAGTCTGCAATTCCTGTTAAAGCCACTTGGGTC ATAAGAGGGGAAGTAAAAAATGAAGTCTGACTAGAAAATTTCTATTGCAGAGGCCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCAATTTGAATTTAG

WI-7555b	60	T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCCAAAATTTGTAGAGGTC/CJCTA AAAAGAAAGTGATGTTGTGATGATCAGCACTAAGTCTGCACTTCTGTTAAAGCCACTTGGGTC ATAAGAGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCAATTGAGTTGTGATATAGTTTTCATTTGATGTCATTTTGAATTTTCAG
WI-7555	60	T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCCAAAATTTGTAGAGGTC/CJCTA AAAAGAAAGTGATGTTGTGATGATCAGCACTAAGTCTGCACTTCTGTTAAAGCCACTTGGGTC ATAAGAGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCAATTGAGTTGTGATATAGTTTTCATTTGATGTCATTTTGAATTTTCAG
WI-7567b	290	G T ---	---	TGAGCCATCACTAGAAAGGCCATTTTCAACTGCTTTGAAACTTGCCTGGGGTCTGAGCATGAT GGGAATAGGAGACAGGGTAGGAAGGGCGCTACTCTCAGGGTCTAAAGATCAAGTGGGCCCTTGG ATCGCTAAGCTGGCTGTTTGTATGCTATTTATGCAAGTTAGGGTCTATGATTTAGGATGCGCTAC TCTCAGGGCTAAAGATCAAGTGGGCCCTGGATCGCTAAGCTGGCTCTGTTT
WI-7569b	63	T C ---	---	AATGATCCCTTTCCGTCACAACAGGAACCTGACTGGGGCAGTGAAGGAAGGATGGCATTC/CJ AGCGTTATGTTAAAAACAAGTATCTGTATGACAACCCGGGATCGTTTGCAGTAAGTAACTCCAT TGGGACATTGTGAAGGCTTAAATGAGTTTAGATGGGAATAGCGTTGTTATCGCCTTGGGTTTAAATT ATTTGATGAGTTCCACTTGTATCATGCGCTACCCGAGGAGAGAGGAGTTTG
WI-7574c	216	A G ---	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGTCCCTTTTCCCTGTTTGTGTTGCCAAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC/A/GTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574b	216	A G ---	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGTCCCTTTTCCCTGTTTGTGTTGCCAAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC/A/GTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574	216	A G ---	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGTCCCTTTTCCCTGTTTGTGTTGCCAAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC/A/GTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7576c	168	A T ---	---	AATGATGATGATAATGATGATGACGACGACAACGATGCTTGTAAACAAGAAAAACATAAGAGAGC CTTGTTTCATCAGTGTTAAAAATTTTGAAGGCGGTACTAGTTGACACACTTTTGAAGTTTGTGT TCTGTTTGTAAACTGGCATCTGACACAAAAA/A/TGTTGAAGGCCCTTATTCTACATTTTCACTAC TTTGTAAAGTGAGAGACAAAGAAGCAANNNNNNNNNNAAGAAAAATAAAAC

WI-7576b	168 A T ---	---	AATGATGATGATAATGATGATGACGACGACAAACGATGCTTGTAACAAGAAAAACATAAGAGAGC CTTGGTTCATCAGTGTAAAAATTTTGAAGGCGGTACTAGTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTAAACTGGCATCTGACACAAAAAA[A/T]GTTGAAGGCCTTATTCTACATTTACCTAC TTTGTAAAGTGAGAGAGACAAAGCAANNNNNNNNAAGAAAAATAAAC
WI-7577q	77 T C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCAACATAAGTGTTCCTTTCTTAA AAATATGCA[T/C]CAAAATCGTCTCTCATTCTTCTCTGAGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50 G C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCAACATAAGTGTTCCTTTCTTAA AAATATGCAATCAAAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157 G A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCAACATAAGTGTTCCTTTCTTAA AAATATGCAATCAAAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACAC[G/A]TAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48 A G ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCAACATAAGTGTTCCTTTCTTAA TAAATATGCAATCAAAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84 G A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCAACATAAGTGTTCCTTTCTTAA AAATATGCAATCAAAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93 T C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCAACATAAGTGTTCCTTTCTTAA AAATATGCAATCAAAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154 C A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCAACATAAGTGTTCCTTTCTTAA AAATATGCAATCAAAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTA/GIACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTTAAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577i	77 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTTAAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577h	50 G C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTTAAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577g	157 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT ATTGTAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577f	48 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTTAAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577e	84 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTTAAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577d	93 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTTAAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC
WI-7577c	154 C A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT ATTGTAATGIGGCCCTGTTATACATGACACTCTTCTGAAITGACTGTATTTC



WI-7577b	117 A G ---	---	---	AAACATGTTCCCTCTCTTAGCACCAAAATAATCAAAACCCAAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTACTTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTTCAATTTTGTTTACACGTAGGAAGAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTTAATGAGGCTGTTATACATGACACTCTCTGAAATGACTGATTTTC
WI-7577	107 G A ---	---	---	AAACATGTTCCCTCTCTTAGCACCAAAATAATCAAAACCCAAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTACTTTCTCTGAG/GJAGTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTTCAATTTTGTTTACACGTAGGAAGAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTTAATGAGGCTGTTATACATGACACTCTCTGAAATGACTGATTTTC
WI-7619q	106 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACAGAGACTTC/GJCTGTGCTGGGGTGTCTATAC ATGGCAGGAAGAAATGGGGCTCTAAGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACAGAGACTCTCTGTGCTGGGGTGTCTAATACATGG CAGGAAGAATGGGGCTTCJTAAGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCCTC TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACAGAGACTCTCTGTGCTGGGGTGTCTAATACATGG CAGGAAGAATGGGGCTCTAAGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCCTC CGCTTTCTTTTACACAGAAACATAGJACATACCGAGAAACCTATTTC
WI-7619n	237 G C ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACAGAGACTCTCTGTGCTGGGGTGTCTAATACATGG CAGGAAGAATGGGGCTCTAAGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCCTC CGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99 C T ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACAGAGACTCTCTGTGCTGGGGTGTCTAATACATGG TGCAAGGAAGAATGGGGCTCTAAGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCCTC TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACAGAGACTCTCTGTGCTGGGGTGTCTAATACATGG CAGGAAGAATGGGGCTCTAAGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCCTC TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90	C G ---	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCG/GJCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206	T G ---	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106	C G ---	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT CGCT/GJTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150	T C ---	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228	A G ---	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTTCTTCTTACACAGAAACAT/GJ/CACATACCGAGAAACCTATTTC
WI-7619f	237	G C ---	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99	C T ---	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189	T A ---	---	---	ACAAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90 C G ---				ACAAGGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAAGAC AGAGAAGGGCCCAATGGGGTCACTC/GC/GC/CCTTAAACGAGACTCTCTGCTGGGGTGTCTAAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGCTCTCCCTTTTCCATCTTTTCCCTTTTCCCT CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---				ACAAGGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAAGAC AGAGAAGGGCCCAATGGGGTCACTCCCTCCCTAACGAGACTCTCTGCTGGGGTGTCTAAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGCTCTCCCTTTTTCATCTTTTCCCTCTCTCT CGCT/GTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---				ACAAGGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAAGAC AGAGAAGGGCCCAATGGGGTCACTCCCTCCCTAACGAGACTCTCTGCTGGGGTGTCTAAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGCTCTCCCTTTTTCATCTTTTCCATCTTAACTCTCT TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---				CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGATCTGCTTGGC/GTAAACCATCATCGGACCAAAATGTG CCATACTAATGATGAGCATTAGCACAAATTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGGCTGCTGTATTTATAGTAACCAATTTCCCTTGGACTGTTC
WI-7626c	155 C T ---				CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGATCTGCTTGGCATTAAACCATCATCGGACCAAAATGTGCCA TACTAATGATGAGCAATTTAGCT/JACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGGCTGCTGTATTTATAGTAACCAATTTCCCTTGGACTGTTC
WI-7626b	28 T A ---				CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TACTATGTGTTTCTGTAACAAATTGGGATCTGCTTGGCATTAAACCATCATCGGACCAAAATGTGCCA CCATACTAATGATGAGCATTAGCACAAATTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGGCTGCTGTATTTATAGTAACCAATTTCCCTTGGACTGTTC
WI-7626	144 T C ---				CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGATCTGCTTGGCATTAAACCATCATCGGACCAAAATGTGCCA TACTAATGAT/JGAGCAATTTAGCACAAATTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGGCTGCTGTATTTATAGTAACCAATTTCCCTTGGACTGTTC
WI-7689c	134 A G ---				TCCCATACCGCTGATTCTCAGGGTCTCTGCTGCCGCCCAACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCCGAGACCTTCTAGGACGCCACCCAGCAAAAGTTGTTCTCTAAAJA /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGACTTAAT GATAATATTGGTGGCCACAAATAAAATGGATTTATTAGAAATTCATATGAC

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WI-7689b	134	A G ---	---	TCCCATAACCGCTGATTCAGGGTCTCTGCTGCCGCCCCACCCAGATGGGGAAGCACAGGTGGGC TTCCAGTGGTGTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTCCTAA/A /GTTAAGGGCAGAGTCACACTGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATTTGGTGGTCCCAAAATAAATGGATTATTAGAAATTCATATGAC
WI-7689	121	G A ---	---	TCCCATAACCGCTGATTCAGGGTCTCTGCTGCCGCCCCACCCAGATGGGGAAGCACAGGTGGGC TTCCAGTGGTGTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTCCTAA AATAAGGGCAGAGTCACACTGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATTTGGTGGTCCCAAAATAAATGGATTATTAGAAATTCATATGAC
WI-7690	45	G A ---	---	TGGAGAACATTCATCTTGGCGTCACTATTCATCAATGAAGATTAG/AJCACTGAGATCCAGAGAGG CTGGATGACTTGTCTCAAGTTCACCCAGCATGGTAGTGGCAAGAGAGGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCACAAAGCTCAGTAGGAGGATGTTCCAGTGGATGAGGGCCACCAGGAAGCAC AGTCCAAAGGTGGTCCACACATTATCAGCAGCAACACTGTCAGTTCATCC
WI-7703b	164	T C ---	---	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTGGAACAAAGTCAGTCATTGATATGATTCAAA TGCTATAAACCCAACTGATGTAAGTAAATTCJGGTCTCTCAGTTGTTTAAACCTCTAAATTCCT TTCATTTAGGGGTAGCATTTGTGTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156	T C ---	---	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTGGAACAAAGTCAGTCATTGATATGATTCAAA TGCTATAAACCCAACTGATGTCJAAGTAAATGGTCTCTCAGTTGTTTAAACCTCTAAATTCCT TTCATTTAGGGGTAGCATTTGTGTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106	C A ---	---	TAAATGAGTGTGTTGTACCCGTTGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/AJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCAGTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCC
WI-7743d	275	C T ---	---	TAAATGAGTGTGTTGTACCCGTTGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTCAGTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCCAAAG
WI-7743e	106	C A ---	---	TAAATGAGTGTGTTGTACCCGTTGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/AJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCAGTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCC

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WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTGTACACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743e	106 C A ---	---	---	TTAAATGAGTGTGTTGTACACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCTCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCC
WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTGTACACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCTCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743c	106 C A ---	---	---	TTAAATGAGTGTGTTGTACACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCTCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743b	275 C T ---	---	---	TTAAATGAGTGTGTTGTACACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCTCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	106 C A ---	---	---	TTAAATGAGTGTGTTGTACACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCTCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	275 C T ---	---	---	TTAAATGAGTGTGTTGTACACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCTCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7758	144 A G ---	---	---	TGACATTTATTCAAAGTTAAAGCAAACACTTACAGAAATTATGAAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATCAGTATAGTTAAACTGCATTATAAATTTATAACAGAAATTAAGTAGATTTTAAAAA GATAAAATGTGTAATTTTGTATATTTTCCCATTTGGACTGTAACTGACTGCC

WI-7765b	126 G C ---	---	---	ACAGGGCCCTTTGGCAGGTGCAGCCOACCTGCCCTTTGACCTGCCCTCCCTTCATGCATGGAAATTCCTCTCATCTGGAACCATCAGAAACACOCCTCACACTGGGACTTGCAGAAAGAGTGCATGG(G/C)TTAGGGAACAACATCCATCCTTGAGTCAAAAAATCTCAATCTCCCTATCTTTGCCACCCTCATGCTGTGTGACTCAAAACCAAATCACTGAACCTTTGCTGAGCCTGTAAAAATAAAGGTGCGGA
WI-7773b	237 C G ---	---	---	TTAATTTACTGATTCAGAGAACCAATCATTTGATCAGATTATTTTAAAGTTTATCCGTAGTTTTGATAAAAGATTTTCCCTATCCTTGGTCTGTCAGAGAACCTTAATAAGTCTACTTTGCCATTAAAGCAGTAGGGTTTCATGCTTTTACCTTTNNNNNNNNNTTGTAAAGTCTAGTTACCTACTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAAC(G)TTTCGACGTTTGA
WI-7774b	170 T C ---	---	---	TGCAACCTCTTTTCGTGATGGCAGCCTGCTGGTCAGCACTCCAGTAGCGAGAGCGCACCCAGAATCAGATCCAGCTTCGGCATTTGATCAGACCAACAGTGTCTTCCGGGAGGAAACACTTTTITTAATTACCTTTTGCGAGGCACCCTTTAATCTGT(TT)CJATACCTTGTCTTATTAATGAGCGACTTAAATGATTGAAAATAATGCTGCTCTTAGTAGCAAGTAAATGTCTTGCT
WI-7785c	165 G ---	---	---	GCAGAGACCTTCCAAGGACATATGCAGGATTCGTATAGTGAACATATGGAAGATTAGAAATATTTATTGCTGTAATACTGTAATGCATTGGAATAAACTGCTCCCCCATTTGCTCTATGAAACTGCACATTGGTCATTGTAATANNNNNNNNNNNGCCAAAGGCTAATCCAAATTATTATCACATTTACCAATAATTATTTGTCCATTGATGATTTATTTTGTAAATGATCTTGGTGTGC
WI-7785b	165 G ---	---	---	GCAGAGACCTTCCAAGGACATATGCAGGATTCGTATAGTGAACATATGGAAGATTAGAAATATTTATTGCTGTAATACTGTAATGCATTGGAATAAACTGCTCCCCCATTTGCTCTATGAAACTGCACATTGGTCATTGTAATANNNNNNNNNNNGCCAAAGGCTAATCCAAATTATTATCACATTTACCAATAATTATTTGTCCATTGATGATTTATTTTGTAAATGATCTTGGTGTGC
WI-7785	156 - T ---	---	---	GCAGAGACCTTCCAAGGACATATGCAGGATTCGTATAGTGAACATATGGAAGATTAGAAATATTTATTGCTGTAATACTGTAATGCATTGGAATAAACTGCTCCCCCATTTGCTCTATGAAACTGCACATTGGTCATTGTAATANNNNNNNNNGCCAAAGGCTAATCCAAATTATTATCACATTTACCAATAATTATTTGTCCATTGATGATTTATTTTGTAAATGATCTTGGTGTGC
WI-7789c	84 G A ---	---	---	TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCICCCAGGAGGGGCCACCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA(G)ATTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTACGGCCCGCTGCCCTAGGATAT GGCCTCCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7789b	84 G A ---	---	---	TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCICCCAGGAGGGGCCACCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA(G)ATTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTACGGCCCGCTGCCCTAGGATAT GGCCTCCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT

WI-7789	73	G A ---	---	TCTCCCTCATCCAAAGTCTGAATCTCCAAAGGAGGCCACCATCTACAGAGACTCTCCC TGACG[G/A]TGGAAATTTAAGTTAGGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7790b	190	C T ---	---	AATTGTCAGTCACCTCTCAAAACCTTACAGTCTTCTTAAGGTACTCTTCATGAGATTCATCCATT TACTAATAGTATTTTGGTGAGTGGCTTGCCTATGTGCTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[G/T]TCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190	C T ---	---	AATTGTCAGTCACCTCTCAAAACCTTACAGTCTTCTTAAGGTACTCTTCATGAGATTCATCCATT TACTAATAGTATTTTGGTGAGTGGCTTGCCTATGTGCTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[G/T]TCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81	C A ---	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGAT[C/A]GTCAATCAAGAAATTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGACTTTTCTCCAGAAAATCTCCTTGAGGAAAATGTCCAAA TAAGATGAATCACCTAATACCGTATCTCTAAATTTGAAATATAATCTG
WI-7795	81	C A ---	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGAT[C/A]GTCAATCAAGAAATTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGACTTTTCTCCAGAAAATCTCCTTGAGGAAAATGTCCAAA TAAGATGAATCACCTAATACCGTATCTCTAAATTTGAAATATAATCTG
WI-7814c	41	G A ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTTGTATATTTTAAAGAAATAACAGAA
WI-7814b	41	G A ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTTGTATATTTTAAAGAAATAACAGAA
WI-7814	28	G A ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTTGTATATTTTAAAGAAATAACAGAA

WI-7830d	150	C T	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGCTGCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAAATGTACACATTCATTTGATAAAAATTAATTTGTTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACTTTTACTTTTTGCGTGGA
WI-7830c	54	G A	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGCTGCTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCATTTGATAAAAATTAATTTGTTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACTTTTACTTTTTGCGTGGA
WI-7830b	134	G A	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGCTGCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACI G/AJATCCATAACTTTAGTCTTAATGTACACATTCATTTGATAAAAATTAATTTGTTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACTTTTACTTTTTGCGTGGA
WI-7830	44	A G	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGCTGCTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCATTTGATAAAAATTAATTTGTTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACTTTTACTTTTTGCGTGGA
WI-7865e	25	C T	---			CCACTTCCTATCTGATTTTCCCAG[C/T]AAATGAGGCAGGCAATCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTCAGGGTGTCTTCCCACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865d	191	C T	---			CCACTTCCTATCTGATTTTCCCAG[C/T]AAATGAGGCAGGCAATCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTCAGGGTGTCTTCCCACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865c	25	C T	---			CCACTTCCTATCTGATTTTCCCAG[C/T]AAATGAGGCAGGCAATCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTCAGGGTGTCTTCCCACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865b	191	C T	---			CCACTTCCTATCTGATTTTCCCAG[C/T]AAATGAGGCAGGCAATCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTCAGGGTGTCTTCCCACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCACCCAGTAAACCCAAA



WI-7865	25 C T ---	---	---	CCACTTCCTATCTGATTTTCCAGAGC/TTAAATGAGGAGGCAATTCCTAGTCTTCCACAAAACATCTA GCCATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTCTCAGTACGAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865	191 C T ---	---	---	CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATTCCTAGTCTTCCACAAAACATCTAGCC ATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGG ATGCTACTCATAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTCTCAGTAC/TTGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7867c	92 A C ---	---	---	TTCAACACCTGTCTTCACCCCTCCACCATCTGTGCAATCACTTCACCCCTCAGCCTCACTAGTCCCC CTAACAAATACCCCTGTCAAGAGGAG/CGAGTGCAGCTCAGGTGGATTTAATGTGGGTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTTCTTTAAGTAACCATTTCTGTCTTCTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7867b	92 A C ---	---	---	TTCAACACCTGTCTTCACCCCTCCACCATCTGTGCAATCACTTCACCCCTCAGCCTCACTAGTCCCC CTAACAAATACCCCTGTCAAGAGGAG/CGAGTGCAGCTCAGGTGGATTTAATGTGGGTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTTCTTTAAGTAACCATTTCTGTCTTCTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7868c	173 C T ---	---	---	TTGATCGATCTTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CACCCAACTGCTCCCTCTGATCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCAAC/TTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCCTAGAT
WI-7868b	173 C T ---	---	---	TTGATCGATCTTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CACCCAACTGCTCCCTCTGATCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCAAC/TTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCCTAGAT
WI-7868	66 T C ---	---	---	TTGATCGATCTTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT /CTCACCCAACTGCTCCCTCTGATCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACAC AATCATTTAATATTTCCCTGTCTTACCCCTATTCAAGCAAC/TTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCCTAGAT
WI-7870b	85 T C ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTATTAGAAGGG GTGGGGTGGCGGGAATCC/CTATTTATCAGACTCTGTAATTAATGAATATAAATGTTTACTCAGAGGA GCTGCAAAATGCTGCAAAATGAAATCCAAATGAGCACCTAGATAATTTAAACATCATTTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG

WI-7870	76 C T	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAATACTCTGCAGTGATTAGAAGGG GTGGGTGG[C/T]GGGAATCCTATTTATCAGACTCTGTAATTGAATATAAATGTTTTACTCAGAGGAG CTGCAAAATTGCCTGCAAAATGAATCCAATGAGCACTAGAATATTTAAACATCATTTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG
WI-7889c	54 C	---	---	TTAGGTCTCATGCCCCACTCCCCAGGAGCAGCTGGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGCCGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCTGGAGAAAGGACATGGGAATGAATTGAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAAGGCTGTCTTCTCCCAGAGCACAAAG
WI-7889b	54 C	---	---	TTAGGTCTCATGCCCCACTCCCCAGGAGCAGCTGGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGCCGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCTGGAGAAAGGACATGGGAATGAATTGAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAAGGCTGTCTTCTCCCAGAGCACAAAG
WI-7894c	142 A G	---	---	AGCCACCCCCAAATATACTGTTATCCAGAGCTGTATGCTCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATGTTTTGTAATTTATTTGCGTATAC ATTATC[AVG]TATGTAAATTTGCATTTTTTATTGAAATTAIGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G	---	---	AGCCACCCCCAAATATACTGTTATCCAGAGCTGTATGCTCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATGTTTTGTAATTTATTTGCGTATAC ATTATC[AVG]TATGTAAATTTGCATTTTTTATTGAAATTAIGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACCTCAACTATAGAAGACATTAAAGAATC
WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACCTCAACTATAGAAGACATTAAAGAATC
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACCTCAACTATAGAAGACATTAAAGAATC

WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCTGCCACAACCTGGCCATGCCCTGCCATTGAACAGTGAATTAGTTTGATCAAGCCATGGTGA/C/TAACAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAATATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCTGCCACAACCTGGCCATGCCCTGCCATTGAACAGTGAATTAGTTTGATCAAGCCATGGTGA/C/TAACAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAATATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCTGCCACAACCTGGCCATGG/C/TTGCTGCCATTGAACAGTGAATTAGTTTGATCAAGCCATGGTGACACAATAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAATATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900c	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCTGCCACAACCTGGCCATGG/C/TTGCTGCCATTGAACAGTGAATTAGTTTGATCAAGCCATGGTGACACAATAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAATATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCTGCCACAACCTGGCCATGGCCATTGAACAGTGAATTAGTTTGATCAAGCCATGGTGA/C/TAACAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAATATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCTGCCACAACCTGGCCATGG/C/TTGCTGCCATTGAACAGTGAATTAGTTTGATCAAGCCATGGTGACACAATAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAATATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33 C T	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATA/C/TAAGACACACACAGGACACATATATTAAACAGATTGTTTCATCATTGTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGACCTTTTTAAACAACAACTCCAGGCCCTTGGTTGCGGCTGCTGGGTTATTGGGCGACGCGCGTGGTCGTCACTCAGTCGCTCTGTCATGCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901b	33 C T	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATA/C/TAAGACACACACAGGACACATATATTAAACAGATTGTTTCATCATTGTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGACCTTTTTAAACAACAACTCCAGGCCCTTGGTTGCGGCTGCTGGGTTATTGGGCGACGCGCGTGGTCGTCACTCAGTCGCTCTGTCATGCTCTGTCATACAGACAGGTAACCTAGTTCT

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WI-7901	33 C T	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAACACAG ATTGTTTCATCATTCATGTCATATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACTCCAGGCCCTGGTTGGGGTCGCTGGGTATTGGGGCAGCGCCCGTGGTCGT CACTCAGTCGCTCGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901	271 T G	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATAACAGACACACAGGACACATATTAACACAGATT GTTTCATCATTCATGTCATATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGACCTT TTTTAAACAACTCCAGGCCCTGGTTGGGGTCGCTGGGTATTGGGGCAGCGCCCGTGGTCGTAC TCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCTGTGT
WI-7926c	150 C A	---	---	CATTCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCATT TACAATGCAATACTTA[C/A]ATTTTAACTCTTTGTAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926b	28 A T	---	---	CATTCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCATT TACAATGCAATACTTA[C/A]ATTTTAACTCTTTGTAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926	150 C A	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACACCATAAGCAGCCAGCCACCAAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAACACCCAGCCGAGGCCACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGTCATTCAAATCCATAGATTTTGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGGCAGCCAGTGTGCCACCTG
WI-7947b	203 G T	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACACCATAAGCAGCCAGCCACCAAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAACACCCAGCCGAGGCCACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGTCATTCAAATCCATAGATTTTGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGGCAGCCAGTGTGCCACCTG
WI-7947	203 G T	---	---	CATGTGTCATGAAGAGCTAATTTAAAAGCAAGTAAGACTAATTAATTTAAAATAAAAATGCC ACAAATTTCAATTTCTCCTCTTAAGTATTACAATGGAGTTTATCTCTGCCCTAAAAGTGGAGAAAT TGAGTGAATGA[T/C]AATTTTGAATTTAGGATTAAGATCCAAATTTTCCCAACTCTTGTTCCTCC CCATAAAGTTAGGCATGAGGAGGAGCACTCATTAAGGCAGAGACGGGAA
WI-7963b	145 T C	---	---	

[illegible]

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WI-8021b	57	C T	---	---	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATCTCATCTGGAAA[C/][G]GATCCC ACGCTTTAGAACCTTACCACAAGGAGTTTTCTTGAGTGAATCTCAAGTCTTGAGGCAATTCGA ACTGGTCTTTTACATTTGAGATTTCTTTTGGGCTCTTATCAAGTCAGCACACACCTTTTCCAAAG GATTTACGTTGCGGCTTGTTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8021	57	C T	---	---	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATCTCATCTGGAAA[C/][G]GATCCC ACGCTTTAGAACCTTACCACAAGGAGTTTTCTTGAGTGAATCTCAAGTCTTGAGGCAATTCGA ACTGGTCTTTTACATTTGAGATTTCTTTTGGGCTCTTATCAAGTCAGCACACACCTTTTCCAAAG GATTTACGTTGCGGCTTGTTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8024c	206	A G	---	---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCATGTGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCCGATGGCAGTTCCTCATGGGAAGACAGAGAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTCATCACCAACAACCATTTAGCCGCTCTAGCCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAGAGC
WI-8024b	206	A G	---	---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCATGTGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCCGATGGCAGTTCCTCATGGGAAGACAGAGAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTCATCACCAACAACCATTTAGCCGCTCTAGCCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAGAGC
WI-8077	167	A G	---	---	GAATGAGCCTTCTAGCCGAGGGAGCTGCTGCTGTTGTTGGCTGCACATGCTATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCAAACCTCTTTCT AAGAGTCTGGGGTGATGCCCCACAAACC[A/G]TAAATCTCATCAGATGGATTTTATTTAACGTT GTGATTGIGACTTACTTTCCAATCTGACTCTGGCATAACAAGGAAAAA
WI-8118f	114	G C	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGATGTAGCTTGTTG[C/][J]TTTCTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCIGATTCCCTGCTCCCTATTCTTCCT AAAAATCAGACTCATTTGTACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGATGTAGCTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCIGATTCCCTGCTCCCTATTCTTCCT AAAAATCAGACTCATTTGTACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGATGTAGCTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCIGATTCCCTGCTCCCTATTCTTCCT AAAAATCAGACTCATTTGTACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---			TCTAGGTTTAAATCAAAGCAATTTGCANITTTGGATTTTGGAAATGA/C/TJCACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACCTGGCAAAATACAGAATGTAGCTTGTGTTTGTCTTAGCCTTGAAGA TGACCAAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTTGTGACCAGTAGCTCTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---			TCTAGGTTTAAATCAAAGCAATTTGCANITTTGGATTTTGGAAATGA/C/TJCACTCCCTTGCTAAGGAAGC GTACTTCATGCTGTGGAACCTGGCAAAATACAGAATGTAGCTTGTGTTTGTCTTAGCCTTGAAGA TGACCAAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTTGTGACCAGTAGCTCTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---			TTTTCTCTCTCCGCGGGGACCAAGGTACCTTCTGGGGCATACAAATGGCAGCGGGCCTCGGGAAG AGGGGTAGGAGACCGAGCAGCATCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8171c	46 A G ---			TTTTCTCTCTCCGCGGGGACCAAGGTACCTTCTGGGGCATACAAATGGCAGCGGGCCTCGG AAGAGGGTAGGAGACCGAGCAGCATCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46 A G ---			TTTTCTCTCTCCGCGGGGACCAAGGTACCTTCTGGGGCATACAAATGGCAGCGGGCCTCGG AAGAGGGTAGGAGACCGAGCAGCATCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298 T C ---			TTTTCTCTCTCCGCGGGGACCAAGGTACCTTCTGGGGCATACAAATGGCAGCGGGCCTCGGGAAG AGGGGTAGGAGACCGAGCAGCATCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85 G C ---			GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGG[C/JAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAGAGCACTGTCCAATAGAACTTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACACT
WI-8314	78 C G ---			GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTTGAGCACATTTCTTGGGTCTGT TTCTCTATCT[C/J]TAAGGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAGAGCACTGTCCAATAGAACTTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACACT

WI-8321	178	G A ---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGTTACTTTTCAAGAGCTGCTGTATATACTAGTCTCTGAGAAG TCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCCAGAAATGAGATATCTTAGTATCTTTCTTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8321	178	G A ---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGTTACTTTTCAAGAGCTGCTGTATATACTAGTCTCTGAGAAG TCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCCAGAAATGAGATATCTTAGTATCTTTCTTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8332b	123	A C ---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAAATGCGATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGCTTTCCCTTCCCTGTGCAGCCTTAGA/CJACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCAGCAATGCCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C ---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAAATGCGATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGCTTTCCCTTCCCTGTGCAGCCTTAGA/CJACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCAGCAATGCCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T C ---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGCCCTCAGGAAGCTTATAATCATGGCAGAAAGCGAAGG GGAAAGCAAGGACCTTCTCACATGGCAGCAGGAGAAAGAGAAAGGAGAAAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGGAGACAGCAGCTAGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACAGGGCCCCCTCCCAACACGTGGGG
WI-8378	308	T C ---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGCCCTCAGGAAGCTTATAATCATGGCAGAAAGCGAAGG GGAAAGCAAGGACCTTCTCACATGGCAGCAGGAGAAAGAGAAAGGAGAAAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGGAGACAGCAGCTAGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACAGGGCCCCCTCCCAACACGTGGGG
WI-8426	184	T G ---	---	TTTAGCACATATTTAGCATTAAAGCCTCAACGATACAGCAATATGTTACATCTCTTTGTGAAAAACAG TTGTTGTAGACTGTTAAANNNNNNNAATGTAACTCCGACTTGTGCCCTAATAGGATTTGACCNTTAA GAGGNTCTTTTGTGTGGANGGGTGGCTTTGCTTGAACCTCCATCTGT/GJGCTTGTAGCTGGTG AGGCTGGGAGTATGGANGNCCCGGGGCCCTTGGCNATNGNATTCAGTGAG
WI-8450h	61	C A ---	---	TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACT/CJA/JCA TCTTCTATCTTAGTCCAAAGTTTGTGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGCTTAAATGCAATTCAT



WI-8450g	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCCAT CTTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCCTTAAAGA AAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCCTTAAAGA AAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCCTTAAAGA AAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCCTTAAAGA AAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCCTTAAAGA AAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCCAT CTTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCCTTAAAGA AAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A/G ---			CAAGGAAAGCTGTCAGTCTTCATAAACTTCAAGAGGTTACAAAATACGTTATTTTAAAGICTA CAATTCAAGATTAGCATCCAACTACAAACATGATGATACATTCGTCACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACCTTACATCACCATTGTTTACTTGTGAAAACCTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGCAGAGTCTTCA

WI-8461c	105 A T ---	---	CTTCCTCTCCAAAATCTACATGAATAGCTTGAAGACAATATAACTACAACCTTACAAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAAAATCAATTTTT[A]TNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---	---	CTTCCTCTCCAAAATCTACATGAATAGCTTGAAGACAA[T]CJATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAAAATCAATTTTTNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---	---	CTTCCTCTCCAAAATCTACATGAATAGCTTGAAGACAA[T]CJATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAAAATCAATTTTTNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---	---	CTTCCTCTCCAAAATCTACATGAATAGCTTGAAGACAAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAAAATCAATTTTT[A]TNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77 A G ---	---	AATAACATGTTATGAAACAAGCTGGTTACAAGTAGTAGGTAGATGACTTAATTTTGATAAAAAAAT TAAAGAAGCAT[G]AACATGCATATAAAAAATAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATATTTCTCCCTTGTTTTGTCTTTTAAAAAACATTATTTCTGAAAAAATAA ATCAGAAAACATGATCGTGGAGAGAAATTATTA
WI-9439b	101 C T ---	---	ACAGAAATGACCTTATTTGTTGTACTA/AGCCTGTTTAACITTTGATACAAAAGTAACATTTTAGTA CAGAAAATCCCAGCTGTACGCTAGTACCTGT[C]TGTGACACACTGTACCATCTCAGTCCCACCT GCCTGTAACTTAGAAAACAGCCCTACCCCGAGGGTCTCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACITGTACCTGTAAACAAAAG
WI-9439a	76 C T ---	---	ACAGAAATGACCTTATTTGTTGTACTAAAGCCTGTTAACTTTTGATACAAAAGTAACATTTTAGTA CAGAAAAT[C]TCCAGTCTGTACGCTCAGTACCTGTCTGTGCACACTGTACCATCTCAGTCCCACCT GCCTGTAACTTAGAAAACAGCCCTACCCCGAGGGTCTCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACITGTACCTGTAAACAAAAG
WI-9446b	75 T C ---	---	GAAAGCTTGATTAAAGGAGGNTTTATTTGATGTNAACCTACCATCCATAGACTATAAAGANCATTA TAAAAAAAT[C]CCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAAGCAAAACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTGTCCTACTNTTATCATCTGTCTCTGCTTTTGTCTACCTA TGNGAACTGGACACTATCTGTGGCAATATTGT

WI-9446	75	T C ---	---	GAAGGCTTGATTAAAGGAGGNNTTATTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTAT TAAAAAAATTCCTCTAAAGNGACACATGCCCAAATGACCAANGNCATAAGCAAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTGNCCTTACTNNTATCACTGTGCTTCTGTCTTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185	A ---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACATTTTTT GAGATAATTATTCTAGATCCAGGCTTTCCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAGTATGTTAATGTCACTT GGAATCTACATGGAAAGCCCAACAAATAACTAAACTTGACTAATGAAG
WI-9497	185	A ---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACATTTTTT GAGATAATTATTCTAGATCCAGGCTTTCCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAGTATGTTAATGTCACTT GGAATCTACATGGAAAGCCCAACAAATAACTAAACTTGACTAATGAAG
WI-9523b	193	C A ---	---	GTGAAAAAGTTTCTATTCCATCATACAATAGATTGTGCTAAGGATCAATTTTGGAGAATGTG CAGCATTCAGAAAGTTGTATCTCATCATGTCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAATTACAAACTATTTAGCCCATGATCTATGGTGATTTCCACACATTGTACATGTA AAAGCTCTTCAGCTTGGAAACAACCTTGCAAGGCAGACTGCATGCACATATAT
WI-9523a	47	G A ---	---	GTGAAAAAGTTTCTATTCCATCATACAATAGATTGTGCTAAGGATCAATTTTGGAGAAT GTGCAGCATTCAGAAAGTTGTATCTCATCATGTCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAATTACAAACTATTTAGCCCATGATCTATGGTGATTTCCACACATTGTACAGTGA AAGCTCTTCAGCTTGGAAACAACCTTGCAAGGCAGACTGCATGCACATATAT
WI-9554	202	T C ---	---	AAAAACACAAGTTTCATACATCACAAAAACCTTCCATTATAACACAGAAGTGATTATTACCAGAC AAGCATCAGTGATGTATAGTCCCTTTCCTTCTAGTTGTTATGTACAAATGCTGTAGATAATGCAGCCCATG CAATACACCCAAAGAACACACTAGAGTCTACACCCCAAGTACAAATATGATAAAGCAGCCCTCTGCAAGTG GTTCGCTGGATACCACTAAGAAAGTCTAGTGCAGCCATGTTGGTTATGATTTT
WI-9555	97	G A ---	---	CCAAAAGCCAAACCATTCATATGTATGGATTTCATAAAACATTTATGATCCTTTTGTAGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAACGAGTCTGAAAAATCAATTTCAAGGGACTCTTTAATCA GTTAAATATCTGCTTTAGAAGGCACAAATGATCATCTTCAGATTAAATACAGGTAAGTATTCAG GGNTAAATGGTACAAAAAAGGCTGTAACTCTTTTNCCTCATTGATCACA
WI-9625b	172	A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCTTGGGAAAAACCTTGGAAAAAACAACACGCACA TAAGTATCATAACTGAGGTTGTGGACAAGTTACTTCTAATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTTAAAAAACAACACTGACAAATCTTTTC

WI-9625	172 A T ---	---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTGTATCTNCTCCTTGGGAAAACTTTGGAAAAAAACACGCACA TAAGTATCATAAAGTGGGTTGGGACAAGTTACTTCTA/TGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTTCATTTAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	---	TTTTTCGAGATCAAGAGCTACATTTTGGTTAGTGTACTACTATACCTTTTTCATCCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTGTAAACAGTGTATGTAGACCTAAAAATCCAAAGCT TACAACT/C/TGTCTTTACCTGATACATTTATCCATTTACTTTTCATTTGGATTTTAAAAATGTTA ACTTAATAGTCTCTTTTCAGATGTCCTGCTTTTAGTTAATGTGTTT
WI-9676n	114 A G ---	---	---	GGCCACTGTCCAAAGCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCA/G/GATGTGGCTTTCTCGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676m	184 G T ---	---	---	GGCCACTGTCCAAAGCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676l	84 A C ---	---	---	GGCCACTGTCCAAAGCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA C/TTCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676k	202 C T ---	---	---	GGCCACTGTCCAAAGCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676j	92 C T ---	---	---	GGCCACTGTCCAAAGCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676i	173 T C ---	---	---	GGCCACTGTCCAAAGCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9676h	134	C A	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTCTCGCCCG C/AJATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCAGGGTCTCTCAGCTTTAAAGCCTTGGATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTCTCGCCCG ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG C/TJAGGGTCTCTCAGCTTTAAAGCCTTGGATCCTATGCATTGTTGTTT
WI-9676f	184	G T	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTCTCGCCCG ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGATCCTATGCATTGTTGTTT
WI-9676e	173	T C	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTCTCGCCCG ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGATCCTATGCATTGTTGTTT
WI-9676d	134	C A	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTCTCGCCCG C/AJATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCAGGGTCTCTCAGCTTTAAAGCCTTGGATCCTATGCATTGTTGTTT
WI-9676c	114	A G	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTCTCGCCCG CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGATCCTATGCATTGTTGTTT
WI-9676b	92	C T	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTCTCGCCCG CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGATCCTATGCATTGTTGTTT
WI-9676a	84	A C	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGTACCAAGNCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTCTCGCCCG CCCATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGATCCTATGCATTGTTGTTT

WI-9738b	40 C A ---	---	TGGACCAACACAGACAGATGTATTCCTGGGCGCTGTGTA/C/A/JATTACAAC'TCATTGATCACATGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGTAATAAGTACTCCACATTTCCCTTTGAGTCAACAAAAGACTCTGCTTGTACACCTGCCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTATCTTTTATTCTGTCCTTATGTTGGGGCACATGCTGTATTGCTGTC
WI-9738	40 C A ---	---	TGGACCAACACAGACAGATGTATTCCTGGTGCCTGTGTA/C/A/JATTACAAC'TCATTGATCACATGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGTAATAAGTACTCCACATTTCCCTTTGAGTCAACAAAAGACTCTGCTTGTACACCTGCCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTATCTTTTATTCTGTCCTTATGTTGGGGCACATGCTGTATTGCTGTC
WI-9756	47 A ---	---	ACTGAAATGTAAATGGCCAAGCACCCAGGACCTTAAATCAATAAGAAGTTAATCTGTGGGAAAAAGTAAC'TACAAAAGCATCTAAACAAGAGCAGGATGTGATGTAAATGTGTCCTTATCACTTTTAGTCAGTAAGATAAGAAAGCCCTGGTGTAGTATCCACTTCCACAACACACAGAAATATACACTTTTGGAAAGATTCACACTTAACCACCTTGATCTTCACCTTTTATGATTTAAACTCTCCGIGG
WI-9758	135 A G ---	---	GATGGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAATAGGAAACTGGGAGAAATCAATTCAAAGAAGAAATCTTGTTCGCAAGGTCATTTTATACTATTTAA/JA/JTAAATAACTCTGGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAACCGCTGGTTTTCTAAATATTACG
WI-9778	127 G A ---	---	ATTAAATCCAGGCAGCGGGGAAATGGATACCTTTTATATGCTCTGTACCCAACTATAAACTTTTGGTTCTCATGCACCATTTTCAATTTTGCCTTCTACTCCAGTACCAGTATTTACCAATTTG/AJCTCTCATAAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGGAAATTTCTCTATTACACACTTTGCCTCAAGAATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116 C A ---	---	TCCTCCCTTTGCTCCTCATGCCCACTCCCTCAGCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGTCCATCTGCATCAAAATCACCTGCAGGAC'TTGCTGACAAATGCAGTTT[C/A/J]GGATCCCACCCAGGACTCAAAAAAACTAGGAATGGGAGAAAGAGGACCTGGAA'CGGTGTGCTAGCAAGCCCCCAGGTGGTTGTAAAGTGGACTAAAGTTTGAGGACCAGACATGGAAGGTTGGCTTTGGC
WI-9841	101 A G ---	---	TGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGATATGAAATTCATTTTGAATGAATAAAATATAC/JA/J]GTGTATGTATATATACTTATTAAACATTAGGATTATACACACAATAAAACGCTGTAAAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGATTGAAAGAGGGGATGTGTTACTTGATATGCTGTG
WI-9880c	222 G A ---	---	GAAC'TAACACCTTTCTGCATGGAATTTTCTTGATTTTGGCAGTTAAACAATAAAATGTTATTAGATCCTGGTGTCTGTGTGGGTTGAGTTTTTATGATATCTCCTGTAGACCCATAAGGGAGGCTGTGAGTTGTTTCTACATCCTTGGACTATATAAGATCCCTTTTAAAAATATATTTTATATAAGCACATGAAATGGAATGAAATAATGA/JA/JTTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	C A ---	---	GAAC TAACACCTTCTTGCATGGATTTTCTTGATTATGGCAGTTAACATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTGGAGTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGAC(A)ATATAAGATCCTCTTTTAAATATATATTTTATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T ---	---	GAAC TAACACCTTCTTGCATGGATTTTCTTGATTATGGCAGTTAACATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTGGAGTTTATGATATCTCTGTAGACCCATAAGGGAGGCTG TGAGTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATATTTTATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T ---	---	ACACTGCAGGCACTCCAAATCCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTTAAAAAACAAACGCCCCAGTTATCACAGTTTCINTTTTTGTC/TCACC ATTTCCATAACAAAAAGAGCTACACAAAAATNGGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCATGAATAATGATTCCAAA
FB25G10b	109	A G ---	---	TCCCTCAATGACAGATGAACATAATTTCTCTGGGTAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAAATGGA(A)GJTGATTTTAGATCCTCCCCAG TGACAAGTAACTGAACTGACCATATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
FB25G10	109	A G ---	---	TCCCTCAATGACAGATGAACATAATTTCTCTGGGTAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAAATGGA(A)GJTGATTTTAGATCCTCCCCAG TGACAAGTAACTGAACTGACCATATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
IB3071	102	C A ---	---	ACAA CGCTGAACCTTCCATAACAGTCAATGGTACAGTCAACATCACATGTACAGAACACACAATTTA GATGAAC TGAATTAAGNTAAATAAAATAAAAT(A)CAATTTTCAGNAAACAAAAATCAAAAC ATTAAGN TCCCTGNATATCTTAAACCCCTAATGAGATTTCACCTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCCTATTAACCCAGTCTAGGGATTCTG
NIB551	161	C T ---	---	CGTCC TTTCTTTTGAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAA TTGGGTTGTCCC TACTGAGCTTGGGGCCAGGTGTACTTAGGAACCCCAATCCACCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGTCTCTTGACCACATACATGCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGGTAGTGAGAAACCAAAAAGCTTGTCC
S72904	51	G T ---	---	AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGAAGTTCCTTTG/TAATTTGTCAGTTTC ATTCCTGGAAAAATCTTTTGAGTTAAATAAGGATCTTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTCCTCAACCAAGTGTGCTGAACCTTCCCTCTTCTGTCAATTTGGTTGTCTTTAAATA TTGCAAAAGTCTGATGCTAAACAGTATTTGGAGTGTTCAGTGTCTGTA

UTR	115	CT			TATCTTTTATCCTGGGGCCACAGTTCTTGATTATTCCTCTTGTTGTTAAAGACTGAATTTGTAAACC CATTAGATAAATGGCAGTACTTTAGGACACACACAAAACACACAGA[CT]ACACCTTTTGTATGTATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33				CCCTGTAGCAGTCTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37				GCTACTACCACGGCTGCTCGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21				GCCATCAAAATTTCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20				TGCTGGTCACTTCTTCACANGCTGTATTACCTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35				AAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23				AACTCTCACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37				AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANAAACAGTTTTCTTTAATTGTAAAGCGGG CATCG
ESTC117	24				AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAAGTTCCATACAAATTTACAAAAAGC CTCCA
ESTC119	24				TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCCTGATAACAGCCTCTTT
ESTC122	34				GACAAATAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21				GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42				GCAGAGGCATCAGATAAGGCCCTCAGAAAAGCCCGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTGGAACCTGG
ESTC129	20				AGTCACCATGCCAGCCCTAGNATGAGTTTAGTAAGATTTGGTTATGCTGGGGAG
ESTC13	46				GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49				GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAAATGAACANGAGAGCTGAAACAAT CTACACCTGAATG



ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCCCTTAGCAACNCTAIGTTGICAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTTGGCTTCTGTCTCTCANAGTCTCTCTCCATGTGGCAACA
ESTC139	45	---	---	---	AGGAGCACAGCCTAAGGACATGAAGGTCAGAGTTTCTCAGAGAGNGGGCTGGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCCATTTGGTGCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCATGGTTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATACTATTTTATTCATTTTAAATC AAAGANACCATTCCTTCTTAAACAACA
ESTC143	29	---	---	---	GTTTACGAAAAGTACTGAAATGCTATTANTAGCTGAATTTGIGATTTCCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTCTTGACATGAGGTNGCTTTTITAGCAGCATTCGG
ESTC146	20	---	---	---	CATGTCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	TCITTTGGTTGCTACACAGACACTTAAGTACTGTATCGCTGATGCGGCGCTGTGGAGGCCCTG GGGGTGGCTGGCGCTGTCTCTGAG
ESTC149	28	---	---	---	TCAGTTCAATTTATTTGCTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAAACAAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATAATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGCCCATTTTCTTTTAAATACAAATCTACTGGTGTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACTCAATCTCTACATACATACAGTNTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAACTCATGAGCATTTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGGAGCGCAAAACAANCCCTGGCTGCCCTGGGATGGAGCGGGGGCCCTCA CCACCACTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCTCTGAGGCACATCAGNTACGTTGGTCAATTTAGGCGACGGTCTGGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCAGCATGATCATCACCCACAAGGACAGGTT TTCTAGCATTGCTGGTGAGTGGGGGCTGAGCTGGGNGCAGTGGGCAAGTGTCACTGGGCCGTTTG GGACTGGGTTGA
ESTC160	38	---	---	---	---	
ESTC162	36	---	---	---	---	CTCTTGTCGGTTTGAAGTTGCTGTTGTTTCCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	---	TCATTCTCCATAGAAATATTGGTTTTGTAAACANCGAATACAATCCAATATATAACATTAAAAACAATCC GATACATACCA
ESTC169	22	---	---	---	---	GTCTCTGGTGTGCAGGGAATCANITTTGCTGGATTAGAGGAAAGTGCCCGCTGTCTCCATGACTT
ESTC176	23	---	---	---	---	CACCTCTCCCTTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAAATTTTNCITTTATTCTATTTAAATACCTTTTAT TCTCTTTATCCCATAAAAAGGCAACCA
ESTC18	29	---	---	---	---	TCAGACACTGCCGACATCAGCATTGTCTCCTGACAGCTCCCTTCCCTGAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	---	TAGGGATTCCAAGTTGCCTGNNTTAATATAATACATATTACAAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	---	GCTTGACTAGCGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAAITGTCAATTCAGCTTG ATTTTCACTCA
ESTC187	24	---	---	---	---	ACCATGATTGCTCTCACACAAGCATNATCAATGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG TCTATTAAACAGGGTTATGTCACACCNTGTCAACCTCAAAACAGATGATACATCATCTTGTCTTCCAT CTTGC
ESTC189	27	---	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	---	TCCTCAAAATACCACTTTCCCTTAACCTTATCAGTCTAGTAAGCNITTCAAAGGAGGAAAATGGGTTAC CTTTCAGGGG
ESTC197	26	---	---	---	---	ATCTCCAGTGTCTGCTGCCCTCCTCCNGCAAAGTCTCCACAAGCACA
ESTC20	33	---	---	---	---	AAGATTAGGACAGACCGGTATAGTAAGCTCTGNGGAACCTCAAGAATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	---	TTTGGTGAAAAATCCCAATATATGAGTTTAAAAAATAATCATTTANCATCATTAAACAGTACTTTAAAT CAATTACTCTTTTGCCTGCAACAG

ESTC201	35	---	---	---	TCCTACITGGGAGTTTAGCAAAACATTTTAAANCCACATCCAACAGATTGGTT CTGCTGGAGGGAGGACAGCGNCGCGGCTGGTGGCCGCCAGAAAGGCTGGCGTGGATGTT CGAGATGAGCC
ESTC202	22	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAATTTACTGCAACTTTGTAGAAATTTATTTGTGCTAC AAGACACGTTGCA
ESTC203	27	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAGC CTAAGAGTGAAAA
ESTC208	43	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAAGTGAGTGACGGTGACCTGTG GGTAACTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC210	29	---	---	---	CTCCAGAGTCCCTCTCTCTCANACCAGGGGCGAGGGAGTTAGGGAAT TGGCAAGAAATTTATTTACACTAACAAATTAATTTAATCAGAGGTATNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC212	27	---	---	---	TTTTGTCAGTAAATGAGCAATACACTGANTGGAATCTGCATGATTAATAACATTAACAAGTTCAT AAACACACCCCA
ESTC214	21	---	---	---	GTACACATCTCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAAAGGAAGC
ESTC216	49	---	---	---	TCATTGAAGAAATTTATGGGTTTTATCTTATTCTAATTGNGAGAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC217	28	---	---	---	CITCTGAAGCCCAAGAGAGGGGCGAGAANGTAGTCTTGATTAAAAAACAGAAAGGGGAGGAGGA CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAAACACACACACACACACA
ESTC219	32	---	---	---	TGCACGTGTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGTCTCAGAAGGA ATGTGTAGGATCG
ESTC220	41	---	---	---	TTCTACTTTATTTTCATATTTCCACCACNATAACGACTCCTTTAATTTAACTAAAAAACCATACAGGGT TCCTGAAGGG
ESTC223	27	---	---	---	GCTTCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA CAAAAGGGTAGTCATATTTCCCANCAACAGCATGATAAAATAATTCAAC
ESTC224	37	---	---	---	
ESTC225	20	---	---	---	
ESTC226	27	---	---	---	
ESTC227	43	---	---	---	
ESTC228	24	---	---	---	

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNTTCTTCCCTCTATTCTCTATAAAATAAGGAAGCAGAAATCT CC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCNGGCCCTCAATTCATATTTATCTTGAGCCGCTTGGTCAGGTTTGAT TCGCACACTOC
ESTC31	32	---	---	---	ACAGCCCCACAGAACAATTGTAAACAATAATTNACAGTCGGTGATCATTTGTAATATACAAATACAAAG CAATTTCCCTCAGA
ESTC33	25	---	---	---	AGCACTCCAGCTCCTTGACGTTGNGGACCAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAGGGAACCCACCTGGGCTTNGGTCACAGAACCTCAGAGCCCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAAATCATTTGCTGATGGAAGAAACCATTT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTTAAAAATATTTGACTTGTTCCTCCCTTCAC
ESTC45	37	---	---	---	TTTGGAGGTTTGTGCTGGAGTTTGTCTTTGTAAACNCTCTCATCATCAGAGGCTATATATAA CTGTCCGTGGTGAGCCCTGCCGCTGTCCCATGGGCCAGGGAGCCACTGGTGCAGNCCGGGCAGATG TTTACCCCTGT
ESTC50	56	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGGAGGTGGCAGGAAGNAGTGGAGGAAAGGACACCA AGT
ESTC56	45	---	---	---	AGTGGGCCCTCCAGTCCCNCTCTGTGGCAGATCCACCAGTCTGCTC
ESTC57	20	---	---	---	CAACACAAAAAGTGTGAGAAAAAACTTCTCAAAATNGTTCAGACTTCAGGAAAAATGATTTCC ACATGGTAAGGCC
ESTC59	38	---	---	---	TCTGCAGCACTTCACCTACCAATGAGCNTTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATG TGGACTGAACCG
ESTC6	27	---	---	---	AGTGATTTGGCTAGGGGTGTTCTCATCTGTGAATTCACAGCGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC61	57	---	---	---	ACAGACAGCATCACACCANAGGGCCCGGAGGGTGGGGAGACACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC63	20	---	---	---	GAGAGGCTAGTCAGGAGGGAANACCCTCAAGTTTAAATCCCACACTTACTTACTGCTCATCCGT CACTTTGGCTAA
ESTC69	20	---	---	---	AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTCTGAGTTGCANGCAGATGGAGATTTGGACACT G
ESTC7	45	---	---	---	

ESTC72	37	---	---	---	GGGCTTCCAAAATGGGTATTGGGGCCAGGAGGCTGGCNIITGGCGTGACGCCCTAAAAAGTGTGACC
ESTC74	49	---	---	---	AACAAATTCACAGCTACAGGAAATCTAGAACAAAAATCAAAATTCATCACNITGGGTGAAAAAGTTG
ESTC77	40	---	---	---	GAAGA ATGACTTTCCTGTCCTCATCGGAAACCAGAGTTTCCCAGGNGAGCCCTTCCTATCTCGGGTTA
ESTC81	20	---	---	---	GGCTCAGCACAGGGATAAGANCCCCACTCCGCATGTCCOCAGAGGGCAGCACTCCAG
ESTC82	25	---	---	---	TTTCAGATGATGGGGTCTGAGATGINTCCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA
ESTC83	53	---	---	---	GAGCCTGACCCA CAAAATCAAAATACACAGATCCAGATATGTGAACCATATACATATCTATACANCCATTATTTAGAC
ESTC85	28	---	---	---	TTTCACAAACCT TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGCTGTTGGGAGGCTACAGCCTGACCACATTTC
ESTC89	22	---	---	---	TTTGC ATTGCAAGGAAGTGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC90	33	---	---	---	CTGGTCTCTTCGTCTGGCATTCTGCTCCTCCTCNGGCCAGTGTCCACCCCAAGTGTCTTCCCGATGAT
ESTC93	29	---	---	---	CTCCCCCTCCTCAGTTCACAGTGGAGACTANGGAGATTGAGGGCAGGATCC
ESTC95	32	---	---	---	GCACGTTCTTGTCTCCTCTCCAGAAAGTTGNAGACGTCTATTAGTTTGATTATCTGTCG
DWU-100	127	C	T	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAAATTC GTGGATCTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTGACTGTCTCCAIC/TGCCAG ATTCTTATCAATGATCTTTCACCTAAGAAACAGCAAAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGCGATTTTTCACAAAATCAAAAGAAGAAAGGCTTAGCTG
DWU-177	77	A	G	---	TTCCATCCTAGATATCTACTCAAAATAATTGAGACAAGTGTCAAACAGAAAGACGCTTGCTGAA TGTTTATGGC/A/GJGCCCTATTACAGTAGCCAAACGATGAAACAAACCCCAAGCTATATATACCA GATGAAAGGATAAACAAAATGTGGTCCATCCATACAAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTATCCCTACTACACTGTGGAT
DWU-286	213	A	C	---	CAATACCTGGACTATCAACCTTGTGCTTAATCCCTGCAGCATCAAGGTTATCCATCTAAGTGAC ATTTTGAAATTCAGCGGTGCCACCAATCATGCCAGCTTCTGTCAATGAATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGAGCTGGGAAACCAGCCCTATCTGAGTCTCGGCTCCCTCC

-176-

DWU-252	94	A G	---	---	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAAGGCACTTCATGTAAAGTGT CAGAAAGGAGCTACAAACCTACCCCTCA/GJTGAGCATGGTACTTGGCCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTCTGTTGAATGACAAAGTATGTGTTTGTGA AT
DWU-330	85	C T	---	---	GAACATTCCTCTGCAGCACITTCACCTACCAATGAGCATTAGCTACTTTTCAGAAATTGAAGGAGAAAA TGCATTATGTGGACTGA/CJTGACTTTTCTAAAGCTCTGAACAAAAGCTTTTCTTCCCTTTTGCAA CAAGACAAAGCAAAAGCCACATTTTGCATTAGACAGATGACGGCTGCTCGAAGAACAAATGTCAGAAA CTCGATGAATGTGTGATTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231	A G	---	---	GAATGTTAATTGGGCAGGTGAAAAGGTACAGATGTGCTGAGCAGACCCTTTGGTTTTAAAGAG AAGCATATTTCCCAACAGGCAACTGTAGAGGCCAGCTGAAGAGTAAAGGAAAAGGTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAGGAGTGAATGTTGAGGGCCCTTCACCTCCATCACAAGAAAGTC ATTAGACGGTACCAATTCAGTGTCTGTTCTT/GJGCAICATTTTCCCTCTGTC
DWU-1537b	89	A G	---	---	CTCTTAACITTCAGTTCCTCATCTATAAGATAAGGATTTCAGTTGTGATCACAATAGTCAAGTAATC CAGGACCAGAAACCCAGGAGC/GJTGAGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGTAACACAAAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52	C T	---	---	CTCTTAACITTCAGTTCCTCATCTATAAGATAAGGATTTCAGTTGTGATCA/CJTAGCTCAGGTA ATCCAGGACCAGAAACCCAGGAGCATGGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGTAACACAAAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196	C G	---	---	ACCATCTTACTATGGCAGGTAAAGTCCATACAGAAAGCCCTCTCTCCCTGGGATTTCAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGGTCACTGTTCCTTCCCTGCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTG/CJGAGA CCCGCAGACCAACTCCTGAGCTTCTGGGCCCTCTGAGTCTTGTCTC
ESTD-ADAA	184	G A	---	---	ACCATCTTACTATGGCAGGTAAAGTCCATACAGAAAGCCCTCTCTCCCTGGGATTTCAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGGTCACTGTTCCTTCCCTGCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTCTGGGCCCTCTGAGTCTTGTCTC
ESTD-ANT1	160	T C	---	---	TCTCTGTCAATTCCTACTCCATTAGTTCAGGTCAAGTCAAGAACTGGGGCAATTACCAAGTAATTCA TGGACTGCCCAACTCGAAACAAAGGGCGAGTGGAGCAGGAGTATTATGCTACGGGGTTACCTT TTTTTATGGAGGACCGAACTGAGGCT/CJGAGCTCAGATCATCCTGT
EST10398 2b	168	A G	---	---	TGCCTGGGGTGGCAAGGCTGCAACAAAGGAGGCAACCCAGGAGGCTTTTATGAAGGGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTTACATTTGGGGCTTGACTTCCACACGGGAGAG CATGTCTTCTCGGGCCCAAGAGGTATCTACC/GJATAGTGTCTATTAGGCATTG

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EST10398 2a	147 C T ---			TGCCTGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTACATTTGGGGCTTGACTTTCCAAACACGGAGAAG CATTTGTTTCTTTC/TJGGCCCAAGAAGGTATCTACCAATAGTGCTATTAGGCATTTG
ESTD-C7	14 G C ---			ATATCGTGGCCTTA/GC/TTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C ---			CTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACCTTTCAAGG ATAATGGGGCAATCACTTCTTTT/CJCTTCTTTAGAGTCTACCGG
ESTD- GPPK2L	38 G A ---			AGTCTTCATCTGGGTGCCAGGTAGATCCCTTTTACC/GA/JCCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G ---			CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGAGCGGCGGCGCAGGCTCACCTCTATAGTGGGTG TATTCGTCCACAAA/A/GTGCATCTGGATCAGCT
ESTD- HRASa	37 C T ---			CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGAGCGG/C/JGGCGCCAGGCTCACCTCTATAGTGGGG TCGTATTCTGTCACAAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G ---			GGAGGCAAGGAGGTGGGGAGGGGCTGCTGCTGCCAGGTCCCACAGACCAGAGAAGCGGCCTCAGTG TATCCCCACCCCCA/A/GJTGCGGCGCTGGGAGATGAAGAGAGTTGATGCAGGT
ESTD-OTC	18 A G ---			GTGACCTTCTCACTTTAA/GJAACCTTTACCGGAGAAAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAATTTAGGATAAAACAGAAAGGAGAGGTATGTAACA
EST36751 7	36 C T ---			CCAAAGTGTTCAATTTAGCTTTGCAGGTTTAACT/C/JGATTACTTTTCTATTCAAACTCTCTGTA AAATTGAATATGAACCTAGTTTCTGATCTATGTTTCAAGTTAAACAG
ES140562	109 A G ---			CACGTGGAAGGAGGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTCCCCAAACCTTGTGGCTGAC TTTATGGCTAAGAAGTTTTCACCTGGATGCATTAATAACAAAT/A/GJTTTACCTTTTGAAAAATAA ATGAAGGATTTGACCTGCTTGGCTCTGGAAGAGATCCGTACCGTCCCTGACGTTTTGAAACAATACA GATGCTTCCCTTGTAGCAGTTTTCAGCCTCCTCTACCCCTA
EST18288 3	121 C T ---			GCCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGTAGAA GATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCCCTGA/C/JGGGAGCCAGT GTGGACAGCACCCCTGGCTTTCACACCTACGTCCACTTCCAAGGTAAGGCAACCTCTCTGTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31 C T ---			GGGAGTGACAGCTAGACACCAAGGGGGGCT/C/JTACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATCTGG
ESTD-ALB	180 A G ---			AATCCAGCACCTTTAGGAGGCTGAGGCAAGGATATCACAGAGGTCAGGAGTTTGAGACCAGTCTGA CCAACTGGTGAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGATGGTGGTGCATGCCTGT AATCCAGGAGGCTGAGGAGGAGAAATCGCTTGAACCTGGAGGCG/A/GJAGGTTGTGGTGAGCCGA GATGGCACCATTGCACCTCCAGCCTGGCAACAAGAGTAAACCTCTGCTTC

EST70523 3	182	G T	---	---	TTCCGCGAGCCCCCATCTTGGCACCCCTGGTCCCCCTCAGGGGCCACCCCGGGCACTCACCGCTCT CGCTCTCGGTAACATCCGGCGGGCGCGCTCTTGGACACATAGCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGCCCTTGGCAGGGGCCAGCCCTG/TJ/CAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACAGTG
ESTD- APO.12	101	C T	---	---	CCAGGTGTGGGCACGTGCTGTATCCAGCTACTCGGGAGACTGAGGCATGAGATCTTTTGAAC CGGGAGGGGAGGTTGAGTGAGTGACATGCTG/TJ/GCCACTGCACCTCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112	C T	---	---	CAGTGTATCGAAAGCCTACAGGACACCAAAATTAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTACGATCTTTGGCTCACATGAAGGCCAAATTCGGAGAGAC/TJCTAGAAGATACACGAGAC CGAATGTATCAATGGACATTCAGCAGGAACTTCAACGATACCTGTCTGTGGTAGGCCAGGTTTATA GCACACTTGTCACTACATTTCTGATTGGTGGACICTTGTCTAAGAACCCTT
EST74167 6	137	C	---	---	AGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCAAGGAGCTGCAGGGCGCGCAGGCCCGGCTGGGCGGGACA/TJ/GAGGA CGTGGCGGGCGCTGGTGACGTACCGGGCGGAGGTGCAGGCCATGCTGGCCAGAGCACCGGAGAGC TGGGGTGGCGCTGCTCCACTGCGCAAGCTGCTGAAGCGGCTCTC
EST43211 8	132	C	---	---	CGCTGTGTGAGTACCGGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGGAGGCTGGGGTGGG CCTCGCTCCCACTCGCAAGCTGGTAAGCGGCTCTCCGGGATCCGATGACCTGCAGAAAGCGCC TGGCAGTGTACAGGGCGGGCGCGAGGGCGCGGAGCGGCTCAGGGCCATCCGGAGGCGCTG GGGCCCTGGTGGACAGGGCGCGGTGGGGCGCGCCACTGTGGGCTC
ESTD- ARSB	126	A	---	---	GGAGAAATGGAGCTGTGGAGGAGGCGTCCGAGGGGTGGGCTTGTGGCAAGCCCTTGCTGA AGCAGAGGGCGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAACCATCAGTGAA GGAGGCCATCCCCCAGAAATTGAGCTGCTGCATAATATTGACCCCAAC
EST36770 4	144	C	---	---	TGTAGCCAAAGTCACCTGCATCATCATTTGGCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATACCTGGGTTCCCTTCTTCTGATCAT TCTTACAAGTTACTCTTATTGGAGGGCCCTAAAGAAGGCTTATG
EST26021 1	137	A	---	---	TAATGTAAGCTCATCCACCAAGAAAGCTGCACCATGTTTGGGTTGAGTGCATGTTTCGAAACCTGT CCATAAAGTAATTTGTGAAGAAAGAGGAGCAAGAGAACATTCCTCTGCAGCACTTCACTACCAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTCTTTTGTGCAACAAGACAAAGCAAAAGCC
ESTD- BA511	29	A/G	---	---	GGGCAACATAGTGAACCCCATCTCTACA/G/AAAAATACAAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAGCCAAAGTGGTCCACTGCA



ESTD-BCL2	116 A G ---	---	AGCTGGATTATAACTCCTCTCTCTGGGGCCGCTGGGGTGGAGCTGGGGCGAGAGTGCCGTT GGCCCCGTTGCTTTCTCTGGGAAGGATGGCGACGCTGGGAGAAQ/GJGGGTACGACAACCGGG AGATAGTGATGAAGTACATCCATTATAAGCTGTGCGAGAGGGCTACGATGGGATGCGGGGAGATGT GGCGCGCGCGCCCGGGGGCGGCGGCAACCGGGCATCTCTCTCTCCCA
ESTD-BCR	69 C T ---	---	CAGTGGCTGAGTGGACGATGACATTGAGAAACCCATAGAGCCCGGAGACTCATCTGCGCAAGA GA/C/TCAAAGAGGTGAGCTTCTGTGTCGCGGAAAGGAGGAGGTGACAAGCTAACTCTGCTTC AAATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCTTGGCACA
ESTD-BRCA1aa	119 C T ---	---	AAGAAAGAGAACTAGAAACAGTTAAAGTGCTTAATAATGCTGAAGACCCCAAGATCTCATGTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCA/C/TTGGTACCTGG TACTGATTATGGCACTCAGGAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACA GAACCAATAAAT
ESTD-BRCA1bb	139 A G ---	---	ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCATGTCACTGAAAAGAA ATGGAAATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAG/A/GJGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA GTATTAAATGAAA
ESTD-BRCA1cc	126 A G ---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTTGCTGAAATGACATTAAAGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGA/A/GJAGGA GAGCTTAGCAGGAGTCTAGCCCTTCACCCATACACATTTGGCTCAGGTTACCGAAGAGGGGCCA AGAAATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
EST512120	122 A C ---	---	ATCCTGAGCTCGCCAATAGCTTCTGTTCTACTTCTCTCTCCACAAGCCCCAATTTCACTTTCTCA GAGGAATCCCAAGCTTAGGAGCCCTGGAGCCCTTTGTGCTCCCACTCAATACA/A/CJAAAGGCCCT CTCTACATCT
ESTD-C1R	40 A G ---	---	ACACAGGTGCTGGCACTGGGGTGGGATCCTCCTCCCTJ/GJATTGCTCCGGGAAGCACATTCTAT CAA
ESTD-C1R	40 A G ---	---	ACACAGGTGCTGGCACTGGGGTGGGATCCTCCTCCCTJ/GJATTGCTCCGGGAAGCACATTCTAT CAA
ESTD-C6	31 A C ---	---	CCCAGTCAGTTTGGGGACAGCCATGCACCTG/A/CJGCCTCTGTAGCCTTCAACCATGCATTCCATC TAAGCTCTGCAAAAT
EST201182	119 C ---	---	GTCCGAATCCTCCTCTGAAAGTGGCCGGTTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGTGAGGGGCTTGAAGCTGGGAGTGGGTTTAGGACGCGGCTCTGCGTGCATCCTAAGCTCT GAGAGCAAAACCTCCCTTGAAGCTGGGAGTGGGTTTAGGGACGCGGGTCTCTGCGTGCATCCTAAGCT CTGAGA
EST530186	67 A G ---	---	ACAAATCCAGGTCACACATTCAGAAAGAGGAGGGGTGGTCAAGTGAAGTCCAGTAATCCA J/VGJGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC

ESTD- CB22	119 C T ---			GGCAAGTTTTATTGATAGAGAGGAATCAAATATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAAATGGCAATGGCAACCCATAGGG[C/T]GGGATACAAAAG ACAGCAAGGAAGGGGTAGAACCATCAAAGAGGAATAGGCTGGTACCCCAAAGCAAGGAGGACCT AGTAACATAATTGTGCTTCATTATGGTCTTTCCCGGCTTCTCTCACACAC TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCTTTCCCGGCTTCTCTCACACATACAGAGGCCCTACAGGACCAGACAGCT CTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAACGTTGTTCCACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAA ACCAAGGACCAGACAGCTCTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTGGTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAG GCCACACTGGTATGCTGGCCACAGGCTCTACCCCGACCATGTGGAGCTGAGCTGGTGGGTGAATGG GAAGAGGTGCACAGTGGGGTCAGACAGACCCGACGCCCTCAAGGAG GTTTCTTTCAGACTGTGGCTTACCTCCGGTAAGTGAGTCTCTCTTTTCTCTATCTTTCGCGCTC TCTGCTCTCGAACCCAGGCGATGGAGATCCACGGACACAGGGCGTGAGGGAGGCCAGACCCCTG TGACAGGTTG/GCCTACATGCTCTGTCTTGTCACAGAGTCTTACAGCAAGGGGTCTGTCTGCC ACCATCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCGGTG TTTTCTGTTTCCCTGAAGATTGAGTCTCCCAACCCCAAGTACGAATAGGCTAAACCAATAAAAAAT TGTTGTTGGGCTGTTGCAATTCAGGAGTCTGTGGAGTCTGCTCATCACTGAC[C/T]TATCTTC TGATTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCT GCTTCTCCTGTTTCATCTGATGGAAGTCTCTCAACACCATTTCCATACC TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGCGAGGTATATGA/ATATGTA TTTCTTAAACAATAAACTTGAAAGTCCAAAATTACTCTTGATCCATGCACTGCAGAATAAATGTTA TTTTAGCTGTGAGAAAACAATACTAATCTTGATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGTA TTGCCAATAAGCAGTAATAATTTGAGAGGAATCTGTGTTCAATGCAAGTAG CAGGCCAGCGTGGTCGAGGTGGTCACCATCCCGGACAGAGAACAGGTCAGCCACCATATGC[AG/CA GGTCTCATCATTTGAAGCTGCTCAGGGTTCCTTGGCTGAGCAGGGCCGAGAGCATACTCGG AAAAAACAATTTAACACCTTTTCAATCATATACACCATATACCATATG/CJATTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCCAATTACTTGCAATCTAAAATGTCATAACTGATTAATGCAAGTTCAACAG ACAAGTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCCA TATCTGCATGTC CATCCCCAAGCCCATCTCTTAGCCACTGGCATTTTTTCCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGATGCCATGGGAAAGGCTCCTCTGGGGCGGTG GGGTTGTGGCTATGTGGTGTCTGTGTAG/C/TGGGGGCTTGGTTTCAGTTGCACTATTGGGTT ATTGCAAGTTGCTTGTGCTTCCACCTGAGCGAGGCTC
ESTD- CB23	136 C ---			
ESTD- CB24	145 A ---			
ESTD- CB25	146 A G ---			
ESTD- CB27	125 C T ---			
ESTD- D4S338	59 A T ---			
ESTD- CYP2D6	61 A G ---			
ESTD- D11S1873	40 A C ---			
ESTD- 117S33b	169 C T ---			

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ESTD- D17S33a	75 C T ---	---	---	CATCCCAAGCCCATCTCTTAGCCACTGGCAATTTTGGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCTACACATCCAGGGGCGCCCTACCCCTTTGTAGTCCATGGAAAGGCTCCTCTGGGGCG GTGGGTTGTGGCTATGTGGTCTTTGTGTAGACGGGGCTTTGGTTTCAGTTGCACATATCTCGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---	---	---	TTTGAGACCACCTGGCCCAACATGGCGAAATCACATCTCTACCAAAATACAAAATTAGCTGGGTGT GGTGTACATGCCCTATCGTAATCCAGCTACATCGGAGGCTGAGCAGGAGAAATGCTTGAACCCJA /GJGGAGGCAGAGCTTCAGTGAGCCCAAGATCACACCCTGCACCTACAGCCTGGGTGACACAGTGGA GACTCIGICTCAA
ESTD- D3S11	44 G ---	---	---	AACTGATTAGAACCTGAAAATACATATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAAATCCAAATAAGTACACTGTATAAAGAAATTAACAGAAATCATATTGT TTATCAAACTATTTATCACTTATTTATTTGTTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	---	AGGTTCCACATTATGCTGATGTTTGTGCTGATGTTTCQJ/GJGGAGCCTTGATGTCATTTCTATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTGTTATTAATTCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGTAGCAGAACATTTCTGCG TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCTCC AGAAGTGAACATACTGCTCCTAGAACCCAGAGTACATCTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTGGAAGGATGCTGTTGGT
ESTD- D3S2a	248 G ---	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGTAGCAGAACATTTCTGCG TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCTCC AGAAGTGAACATACTGCTCCTAGAACCCAGAGTACATCTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTGGAAGGATGCTGTTGGT
ESTD- D7S399	83 A G ---	---	---	TGAATCTTAATTGCTATCTCTACAAATGTATAATCTGAACTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJ/GJGCTCTCTACATCATCTTTTCAAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAAACATGACAAACATTTTTC
ESTD-DMb	146 A C ---	---	---	GTGGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACGTTGGCTCAAGCAGCTGCTCGGGCTCCACT TCCATGGGTGGGGCTGGGACCTCAGTCTCCTGGGAGAGGAGGAGGTGGGAGGGAGACA GAATGCTGATTJAVJCTGTGGTGAGAACCAAGTCTGCGCTGTGGGTAGGGGCGAGCTGCTTCCAAG ACCTCCTGATTTGAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD-DMa	66 C G ---	---	---	GTGGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACGTTGGCTCAAGCAGCTGCTCGGGCTCCACJ GJTTCATGGGTGGGGCTGGGACCTCAGTCTCCTGGGAGAGGAGGAGGAGGTGGGAGGGAGAGA CAGAAATGCTGATTATCTGGTGGAGAACCAAGTCTGCGCTGTGGGTAGGGGCGAGCTGCTTCCAAGA CCTCCTGATTTGAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAGT

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ESTD- DRD1	154 C T ---			TCCCCAGCCCTATCGGTGCATATTGGACTATGACACTGACGTCCTCTCTGGAGAAAGATCCAAACCCATCAC ACAAACGGTACAGCACCCCAACCTGAACCTCGCAGATGAATCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGIC/TTCGCTATTAGAAACTAAGGTAC
ESTD- DRD2	144 C ---			TCTGCCTTTGTGAGGAGGCTGCCCGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTACAGCCCATCCACCCAGCCACCCAGCTGACTCTCCCCGAGCCCG TCCCACACAGGTCTCCACAGCACTCCCGACAGCCCGCCCAACCCAGAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---			AAGACGATGCCAGGATAGCGCGCAGTAGGAGAGGCGCATAGTAGGCATGTGGCGGGCCTGGCTGG CACCTGTGGAGTCTCTGCCCCACAGGTGTAGTTCAGGTGGC/TACTCAGCTGGCTCAGAGATGCC ATAGCCACAGGGAGGTGGTGATGCCAAGGGGCTCCTGTGAGGAGA
ESTD- ERB2	93 C T ---			TCTTTCAGGATCCGCATCTGCCCTGGTTGGGCATCGCTCGCTAGGTGTACGGCTCCACCAGCTGG GGTGAGGGGTGGTGGTCAGTCG/TJGGGGCCGGTGCAGACCCACCGGGCTGGGAGGACTTCA CCCCGCTACCTCCGTTCTCTGCAGCAGICTCCGCATCGI TACT
ESTD- ETS2	43 A G ---			ACTCACAGTGTCTTTAAGTGAATAATGGTCGAGAAAGAGGCACC/AG/GGAAAGCCGCTCTGGCGCCTG GCAGTCCGTGGGACGGGATGGTCTGGCTGTTGAGATTCTCAAGAGGAGCGAGCATGCTGTGGACACA CACAGACTATTTTAGATTCTTTTGCCTTTTGCACCCAGGAACAGCAATGCAAAAACCTCTTTGAG AGGGTAGGAGGGTGGGAAGGAACAACCATGTCTTTTTCAGAAAGTTAGTTTG
ESTD-F9	111 A G ---			AGATCCTGATGATTTTTTCCCTATTTTTCTAAATGTTTTACAGTTTGAAGTTTTAGATTATGCCCA TGCTCCATTTGAGTTAATATTTGTGTAAGATATGATGTTTAA/AG/GTCAAACTTCATTTTTTTTTCC ATAGGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAAC
EST68787 5	144 A ---			CTTCTATGGGATTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAAAAG GAAGCTTGACGCTCATGACAAATTTGAAGCTGACAAATTACACAAGAAAGGAATAATTCACAGTCAA AGAAATCAAGCACTTTTCGAACATTGAAGTTGTTTTGAACCTTGGTGCACCTTTAATTACAACTAG CAGACGGAACCTGAACCTCAGGGTAAGAAAT
ESTD- GCDH	200 C G ---			CGCAGACCCGGTCAGTGTGGGGTCGGGAGTGTGGAGGGAAGGAGGGAACCTGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTGACAGAGAAAGCGGGAGAAACACAGAGCCAACTGGCTAA GTGTAAAGGGACCTCTGGTCGCACCGTGTGTTCTGCTGCCCTGTTTACGCTGTCTGTCTGCCGCACTC/ GIGACTCTGTCCCGAAATCCGAGAGCT
ESTD-GCK	88 A G ---			GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGGCCCTCTCAGGA/AGJACACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCGAGCGGCGCTGAGCCCCAGGAAAGCAGGCTAGGATGTGAGAGACACAGTTC ACCTGCAGCCTAATTACTCAAAAGCTGTCCCCCAGGTACAG

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EST34088 2	62 A T ---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGGCCACAAAGAGACCGGCTC[A/T] AGGATCCCAAGGGCCCAACTCCCGAAGCACTCAGGGTCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGTCAAAACCCAC[A/G]GGCATCA TTGAACCAAGTTTCCGTCAAGACTTGAATTCAGGTAAGTGCATGGTTCCCTAGG
ESTD-HT2	154 G ---	---	GGGCTAAATTTCCGAGCAACTTTGCAATAGACTGTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAGATGTTACAGTTGTCAGAGATAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAACAAGACACACCTT
ESTD-HT5	149 C ---	---	AACACAAAGCCCCAGCGAGAAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTGCCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGTTTCTCTCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATCTCTACAAAATGAAA ACATTTCTGCTCTGTAATCCCTCGAAAAGGTTCT
EST37382 5	124 A G ---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCTCCCTTGGA CTTTGAGTCAAAATGGCTGGACTTGAGTCCCTGAACAGCAAGAAAGAAAGG[A/G]CCCCAGA AATCACAGGTGGGCACGTCGCTACCGCCATCTCCCTCTCACGGGAATTTTCAGGGTAAACT
ESTD- IGFBP1	43 C T ---	---	ACCCAGTGGAGCCGCTCATTCACCGTCTTGGCAGGAGGTGC[T/CT]GGGAGAAGGAAGATG TTCCAGGGCACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ---	---	TTTACTATTTCAATGGATACAGAATTTGGGAGTCACTATATTCCTATGAACAAAAATTCAATTT CAGTGTAAAGTAATGTTGCCCTACATTTGTGTGAGTGACGGGCAGTGGTGCAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAAATACTTCACAAAATACTAATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	110 A G ---	---	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATTATTATTATTATTTATTTTGTG AGATGGAGTCTGGCTGTCAACCCAGGCTGGAGTGAGTGGC[A/G]CAATCTCGGCTCACTGCAAGCT CTGCCCTCGGGTTCATGCCATTCTCTGCTCAGCCTCCCGAGTAGTGGGAATACAGGCACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCAACCGT
ESTD-IL1B	99 A G ---	---	CCACTTACAGATGGATAAATGGGTACATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCCCTC[A/G]GGAGCTCTCTGCAATTGCAGG
EST74082	134 A T ---	---	TCCAGGGTGGCTGGACCCAGGCCCCAGCTCTGCAGCAGGGAGGACGTGGCTGGCTCGTGAAGCATG TGGGGGTGAGCCCAAGGGCCCAAGGAGGACCTGGCCCTTACGCTTACGCTCAGCCCTGCCTGTCT[A/] TCCAGATCACTGCTCTTCTGCCATGCCCTGTGGATGGGCTCTCTGCCCTGTCTGGGCTGTCTGGCC CTCTGGGGACCTGACCCAGCCGAGCCCTTTGTGAACCAACACCTGTGGG

EST45311	151 C T ---			GCCCTCCTCTCTCCAAATCTGTCCCTATAGTTTTCCTCTATTAAAGTGAACATGACATGCATTCITTTAGT GGATAGATGCACACAACACACAGCCCAATATGGGGAAGGATCCACGTGTGTGGCCATATTTGTAACA CATTTTCGTCAAAT[C/JACCTCTTTTCAATTAACAGCCCTATTCAATGGCCITTTTCTTTTCAGTA GTACATACACATCTGTGTCAATTTGTTGAAT
EST65258	80 A G ---			TGCCCATCAGCGGCGGAGACATGGCTTGCACAGCTCTTGAGGATGTCACCAATTAACCCAGAAAT CCAGTATTTTCQJA/GJCCCTCAAATGACAGCCATGGCCGGGGTCTCTGGGGCTCGTCGGG GGACAGCTCCACTCTGACTGGCACAGTCTTGATGGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216	26 A T ---			ATGCAGGATGAAGGTGACAGGGAGGJA/TJGAGGGCCAACTGTCTCCAGGGCCTGCAGATGTGG CTGGACTATGGGTTTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	149 G T ---			ATACTAGTACAAAGTGGTAATTTTGTACATTACACTAAATTAATGCAATTTGTTTAGCATTACCTAA TTTTTTCCTGCTCCATGCAGACTGTTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAG TTTTTTTTCCTC[G/JAAGTGCCAGTATCCAGAGTTTGGTTTTTGAACGTAGCAATGCTGTGAA AAAGAACTGAATACCTAAGATTTCTGTCTGGGGTTTTTGGTGCATGCA
ESTD- KRT10b	183 C T ---			CCAAAGTTAAATAGTATTGGAGTATCTGAGAAATTTCCATGICAGITGTTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTTAAAGTAAGTCTAAGGTTTTTCCATTAAACCACATTAATCTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAG[C/J]TGCTTTTAAATAGT CTCTGCCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT10a	133 A G ---			CCAAAGTTAAATAGTATTGGAGTATCTGAGAAATTTCCATGICAGITGTTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTTAAAGTAAGTCTAAGGTTTTTCCATTAAACCACATTAATCTCTA/J GJGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTC TCTGCCCAGATACATCTCCCTATATA/GTTATAACCAAGTATTGATA
ESTD- KRT8b	231 C T ---			ACCTCACCCCTCCCTTAGCCCGTGGGANGCAGGAAATCTCTCCAAATCCATGAAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCCATAG GCTGCCCTATCTCTCCCGTCTCAGGTTTACCA[C/J]GTCAACATTGACACA
ESTD- KRT8a	21 C T ---			ACCCTCACCCCTCCCTTAGCC[C/J]GTGGGAAGCAGGAAATCTCTCCAAATCCATGAAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCCATA GGCTGCCCTATCTCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
EST75099	82 C T ---			CACCTGTGTGTCTAGATCTCCTCAGTGGCCGCTCTACTGGGTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA[C/J]GGGGGCAACCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGCCCCACC CCTTCTCCTTGGCCGCTTTGAGGTGTGG

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ESTD- LF79	142 A G ---	---	GGGTGATTTTGGGGCTAGTTAATATTTCAAATGTAAACCGTAGCAAAACGCGATTGGTATTTAGA AAAAATAAAATTTCCAAATATGTAGTGTGTATATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACC[A/G]GGAGGGCTCCCTTACCACCCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGTGAGTTATTAGGCATGTTTACCTGTGATTTCTCCCAATCTTGTGGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGTACCCAAATAGGTGAACATGGCTTCGAG AGAGTTG[A/C]ACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA
ESTD- LMP2	35 C G ---	---	A TACACATTTTCTTACCCATTACCTGAAACGACT[C/G]GCAAACTGGAGCCTTTAGGAATGGAGT TGACCTTCCCCAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGGCACCTCACCATCCAGCTTCTCAGCTCTGCCCTGCTGCTGCTGCTGCA AGGGTTTGGCTTAATTCATTCATGTCTCTCATCTTTTAGIC/TAAGCTGTGGGGTTTGTGTTG TTCCTCTGTTTGTCTAGTATCTGACTACTTTTAAATTAATAAAGAGATGTATCTAAACAAAAATAG AGATTGTTATCAGAAGTTCAACAACATTTTAAATAATTTTTCACCTG
ESTD-MCC	45 C T ---	---	TTGTCAGGAGTGTGCTGATGCTGCCTCCCGAGCTCTGTCCCTAGC[C/TA]GAACCTTCAGGACAACGTGC AG
ESTD- METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCGAA TCTCAGGAAGTCTCTGCTTCCAGGGTTTGGTCAAGTTGCTGATTACCT[C/T]GGATTTTCTGACG ATCTTCACTGCTAGAGCATCTGGTTCTCTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAACT[A/G]TACCAGATCCCACAGACTGATGGCTGGT AACATGGACTTGTATATTGTACAAA. AAAAGTTTATTTTCTAAAAAAGAAAAAGAGAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCCT[A/G]GCCCCAAACGCTTATTGTGGT AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGACGAGAAAGATCATTTGAAATCT GAGAAACTTCTTTTAAACCTCACCTTTGTGGGGTTTGTGAGAAAGTTATCA
ESTD- NFKB1	107 A G ---	---	TGTCCTTAGGCCCCAGCCCTGCTTGCTCCTCCCTGGCTGTATCTT[C/A/G]TACTGCAAGAGAACACA GACAT
ESTD- NPPA	45 A G ---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAATTTGGT GGGTTTCTTTTATGTAGGTGATATGGATCTTTTGTGATTATATATAGCAATTTGAGGG ACAAACAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTAACCTTGGCAATAGCATTG[C C/T]ATCCCTGTGGTTTAAATAAAAT
ESTD- NRAS	202 C T ---	---	GCCACCACCCACCCACCCAGCACACCTCCAACTCAGCCAGACAAGGTTGTGACACAAGAGAGCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGG[A/G]GTACGCCGTGTATCATCGAGGCGGCCGGG CACATGGCAGGGATGAGGGAAAGACCAAGAGTCTCTGTTGGGGCCCAAGTCCTTAGACAGACAAAACC
ESTD-PAI1	100 A G ---	---	TAGACAATCACGGTGGCTGGCT

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ESTD-AR	120	A	---	---	CTCTCAGGAACCAACGAGTCTCTTACCAACACGAGCTTATTGCTGTCGAGAGGTACAAACCCGTAGA
ESTD-Per/RDS	74	A	G	---	ACTTCTTCTAACTGTAATTTAGTTAAAGGAATCGAAACGAGTGGCTCTGAGACATGGAGATACGCT
EST68308	5	29	C	T	AATCGACTGGCTTTTCATTAGCTCTGAGAGTGTCTTCTTCTTCTGTTCTAGAACGTTTCTTAG
EST54045	6	39	A	G	GACTGGCAGTTTAAGCTTTCACCTAGGCTTTCGTATACCCATGCC
EST76136	39	C	T	---	ACCTACAGACGTGCTGGATGGTGTGTCACACCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTG
ESTD-SPTB	176	C	T	---	CTGGAGAAGGAGCGTGGGAGACCTGGAAAGGCTT
ESTD-PMPI	88	A	G	---	GGAAAGAGATTAAAGAGCTTGAATTTGGA[CT]AATCTGGTCTTGGAGTGTGGAAGATTTCATGTC
ESTD-RDS	127	A	---	---	TCTGCTGAGTTACAAACAGAAATCCTTATAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT
ESTD-s14544	94	G	T	---	GGAGAAAGTAGACTTTAAAGGTAAGAAAGTAGTATTTTAA
EST52908	0	45	A	C	GGAAATATAAAATATTTAAATACCTCCATTTTGGCTT[AG]TCCCTTTAGTGAAGATGATACCTGC
EST19590	55	C	T	---	AAAAGACATGGCTAAAGTTATGATGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA
EST76136	39	C	T	---	TCTGTTAAGTAAGTACTGTTTGGCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
ESTD-SPTB	176	C	T	---	ATGAACATGGTCTTTAATTTATGATATGTTGTTATAGCTATCTTAAAGGGCTTCTTTTTTTA
ESTD-SPTB	176	C	T	---	ATGCAGAAAGAGGGGAAAAA[AG]GAGCGAGCTGGTGGACAAGGTGTTTTCTCAAGGCTCATAC
ESTD-SPTB	176	C	T	---	AGATTCTGAAAATCATGTCCTCCCTAGAACATTTTGAAGAGGTAAAGTCTTATGAAATATAATCTT
ESTD-SPTB	176	C	T	---	CCCGAGGAATCTGAGAGCGAGAGCGAGGCTGGCTGCTGGAGAGAGGCTGCCGAGACCTGGAAGG
ESTD-SPTB	176	C	T	---	CCTTCTGGAGAGTGTGAAGAGCTGGCAAGGGCAACAGGTGGAGCCGAGGCGCAGACGCGAGG
ESTD-SPTB	176	C	T	---	CCAGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCGAACTGAGAAATAGTGCAC
ESTD-SPTB	176	C	T	---	CCAAAGAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD-SPTB	176	C	T	---	TTGGGAAGTTAGAGCCTATATTAATACGGAATTACTAAGGCAGGACACAGAGGCTTAAATTGAAAA
ESTD-SPTB	176	C	T	---	TATCCCAAAGTTGAAATGTCTCAGTT[CT]CTGTGTGGTTAGATGCAGGATTTATATGATCCGTTA
ESTD-SPTB	176	C	T	---	ACCTCT
ESTD-SPTB	176	C	T	---	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTCTGGAGAGATGG[AC]TGGTGGTCTGCAAGCCCTT
ESTD-SPTB	176	C	T	---	TGGCAATGTGAGATTTGATG
ESTD-SPTB	176	C	T	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAAGATGACATTGATGAGTGAAGATGT[CT]GGCTCAG
ESTD-SPTB	176	C	T	---	GATGCCCGGAAATGAC
ESTD-SPTB	176	C	T	---	TGAAGCTTCTGCCAGCTTGCATTTGTTCTAGGAGAACC[CT]GCGTCATACCTTTATCTATAGCCTT
ESTD-SPTB	176	C	T	---	CCCCTAGGCTT
ESTD-SPTB	176	C	T	---	TGAACACCCCTGTGGTCCGAGCCAGGTGTGTTTCTCTGGAGCCCTGAGGAGTTTGTGCTGTGTG
ESTD-SPTB	176	C	T	---	CAGTCCCCCGGCAACCTGCTGTGTTGAGCCTGGACATACACCTTCACTTCTTGGCCCGGAGAGAC
ESTD-SPTB	176	C	T	---	ATTTACCCACCTGGCCATGTCCCTGGGCTGTTGTGCAC[CT]CTCTGTGAAGACCCCAACCCCTGC
ESTD-SPTB	176	C	T	---	CTCCCCACCCCAAGCCAGTTTCTCTAGCAAGGGCAGGAC



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ESTD-TAT	224	C ---	---	AAATGGTCAGGACCCCTGATCCACAAGAGTGGTACCATTTTCATCAGGGCCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCCCTCACCTAGAACGTTTGTACAACTTTCTCCAGTATGGATGGATTATGATGGGGGG GAGAAGCAAAATTTTAAATAGGACCCATGAGACACATCA
ESTD- THRB	125	A C ---	---	TGGGCCCTTCTCCGGCAGGGTAGACTTCCTTACTTGGCTGTTGATTTCCAAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATACACAGGATC[A/C]TTCAT CCACTGGATTGGCCCAACAAGCTGAGTCCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCTGTGAGCTTCGGATTCTTGTCCCAACCAAGAGAGTCTATGC CAAGGCAGAAAGCTGGTCTCATGGGCAAAATCAATGCTCTCCAGATTTCAG[T]ATCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAGAGGTCATAATAATTGATGTCGTTAAA CATGGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA
ESTD-TYR	122	G T ---	---	AGTAGTGGATGAAGCTAACCGCCTCTCCTCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATCACTGATTTCTTTTACCTTTTACCTTTCTCT AATACAAGCATATGTTAG[A/C]ATTAAGTTCTAGGCATACIT
ESTD- TYRP1	222	A C ---	---	AGTAGTGGATGAAGCTAACCGCCTCTCCTCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATCACTGATTTCTTTTACCTTTTACCTTTCTCT AATACAAGCATATGTTAG[A/C]ATTAAGTTCTAGGCATACIT
ESTD- VB12	148	C T ---	---	TCCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGGTCACAGAGACAGGAACACACAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAAACCCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148	C T ---	---	TCCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGGTCACAGAGACAGGAACACACAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAAACCCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74	A G ---	---	TCCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC[A/G]TGGATGCTGGAATCACCCAGAGCCCAAGGTCACAGAGACAGGAACACACCA GTGACTCTGAGATGTCAACAGACTGAGAAACCCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAGCCAGTCCATCTCTGTAGTCATCATAGTTTGGCTCC CAAGTTGCTCTCTCACTGGAGAACAGGACAGCCAC[AG]TGGCGGGATGGCCGGCGGAGTTT TGGTTGGCGCCACGGCTGTGGCCTCGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGT TTCTGGCCAAAGGAGGGGGGGTCCATGCTGAGATGTAGATGCGGCC
ESTD-VWF	36 G ---	---	AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCTTTGG TCCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACCACTCTCACGTCAGCCCTCAGCACAGATGCTGTTCTATAGGATGACGTGCTGTTTTACAA CATCTCTCCATGAAGAGCACAGAGATTATTTATTCCTGAAGTCCGGATCTATGACTCAGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAAACCACTGCAGAGTACCAG[C/G]TGTGGTGGA AGGAGTGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
ESTD- TNFab	152 A G ---	---	TTCTGCATCTCTGTCTGGAAGTTAGAAGGAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTTCAAGCCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAAAGACCCCTC[AG]GAAATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTTGATG CTGTGTGTCCTCCCACTTCCAAATCCCCCCCCCGGATGG
ESTD- TNFAa	88 A ---	---	TTCTGCATCTCTGTCTGGAAGTTAGAAGGAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTTCAAGCCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAAAGACCCCTCAGAAATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTTGATGCTT GTGTGTCCTCCCACTTCCAAATCCCCCCCCCGGATGG
EST52418 6	113 A G ---	---	CAAAATTACAGGGTCAACTGCTATGATGTGTTGGAGCCCACTCACCCCTTGGTGGCTACAAGATGTGG GGGAGTGGCCGGGAGTTGGCGGAGTACGGGCTGCAGGCATACACT[AG]AAGTGAAAACTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACTCTATTTGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTAAGTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC[AG]GGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAAGAGGTGCGTCTGCTGCCCTGCC CCGGTCACTC
EST51976 7	123 A T ---	---	AGGCAGAAACTGGGCCCCCATGCGGGGACGTGGAGGCCACTTGAGCTTCTCTGGAGAAAGGACCTGA GGGACAAGGTCAACTCTTCTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAG[AT]CTCTCTC CTCCCTGAGCTGGAGCAACAGCAGGAAACAGCAGAGGAGCAGCAGGAGCAGGAGTGCAAGATGCTG GCCCTTTGCAAGCTGAGCTGCCCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTCACTTCTCGAGTTTT CTCTGCCATGTTGCTATTGACGAGCAGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCC[AG]TTAAACATTTCTATGAGCCAGGAGAGATACGTATTTCTGCAAGCCGGGCTATGTG TCCCGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

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ESTD- AT3aa	60	C T	---		AGACCTCAGTTCTCTCTGTAAAGGGAAGTTTGTTCTTGATCTCCATGGGCCAGCIC/TJAGCA CTGGTCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCAGGTGGAGGAAITTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAAAGAGCTGGGGAATGTGG
EST39852 8	106	C G	---	---	CGGCTTCCTCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACCTCTTTC/G/GGGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAGGCGTGTTCAGGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112	A G	---	---	ACCTGGTGTGCTGGTGGTGAACCTGGTCTCTTGGCATTCGCCCTCTCTGGCCCTCTGGCCCTGGG TCCTCCTGGTGTGGTGTGGTAGTCTGGAGTCAACGGTCTCTT/G/GTGAAGCTGGTGTGGTGGCA ACCTGGGAACGATGGTCCCCAGGTCCGATGGTCAACCCGACACAAAGGAGAGCGGGTTACCC TGCCAATAT
EST36027 2	120	A C	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTCATGGCCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCAGTGAAGAACAGCATTCATACATGGATGAGGAGACTGG/AC/JAACCTGAAAA AGGCTGCTATTCTACAGGCTCTAATGATGTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTGTAGATGGCTGCTCTAAAGACAAATGAATGGGAAAGACAA
ESTD- COL2A1cc	112	A G	---	---	AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTCTGTCACCTTC/J/GJGGGTGTTCAAGGTGAAAA GGTGAACAGGGTCCCGTGGTCTCCAGGCTTCCAGTAACTCAACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97	C T	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTGCTGGGACCTGGAAACA/C/JTGGACTCTTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAITGGCAAAGATATACAAATACAAATTTTATTTGACCAAACTATCATGGAACA GCATT
ESTD- CPT2	150	A G	---	---	GCCGCAATGCCCGGAGTTTCTCCAATGTGTGGAGAAGCCCTTAGAAGACATGTTTGATGCCCTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAGCTACCATCACTTCTCTCATGAAAAAC TGGGAGGCCGGGCAT/J/GJGTGCTCATGCTGTAAATCCCAGCATTTGAGAGGCTGAGGCGGGTGGAT CACTTGAGGTGAGGATTTGAGACCAACCTGGCCAAACAT
EST12274 0	135	A G	---	---	CCCCAGTTGACAGCCACTGCTAGACTAAGTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGAT TACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAAAATATCTTCCCTCCTTGGATGAGGTG A/GJTAGTAATGACCGATGGGTGAGAACTGTCTGTCCACTGGAGGATACTATAACTGTGAAGA TAAATCAAGCCACAGAGCTTGCCAGATC
EST76807	91	G	---	---	ATGCTAAGGGGATCGGACATGAAGGACCCCTGTGAGCCGATTGTCTATCTCCAGCGGCCCTGTCTATC CAGTCACTCATCAATGGGCCAGTCAGGCCAGGACTGGCTCCGAGGAGTCACTCACTGCCCCCT GCTGCCATGTGGACTGGTGAAGTTGAGGACTTCTTG

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ESTD-SSA1	111 C T ---			TTACATTTGTGGATTGTTCTTTTGGCTGTGCAGCACCTTTTCAACATGATGTGATGCCATTGTGTCGAAG TTTGGCTTTGGCTGCTGTGTGGGATATTTGAAAGAGATCTTTTGGCCAGTCCCAATGTCTCTAGTA GAGTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTTAGATTTAAGTCTTTAATCCATT TTGATTTGATTCTGTGA
ESTD-RYR1	109 A G ---			CTTCGTACGGGAGGTACGTCCTCCGCCCTTTTCATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTATGACACGCGAGACTTGTCTACTATGAGTGGGGAGCTGTGTGCACTCATGCC CGCTCCCTCTGGAGGCTGGAGCCACTGAGAATCAGTGGAGTGGAGCCACCTGGCTGGGGCCAGCC ACTCCGAGTCGGCATGTCTACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G ---			AAGACCTACGTGAATGTTACATGTGCTTAAAGCCCTCCCTTCCCTTACTCTCTGCTGCTGACGATGTG CGTGGTGTGCTGGAGTAGCCCGGACTCTTGACGGTCGGCATCTGAGACCAGTGAGAAACGCCCC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST4438 7	100 C --- 62 C T ---			GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCCAACTGTGCATGCACGGCTTAACCTCT GCACCAAATGGCTCCAAAGGCCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTAGGAATGGCCC AGCCAGTCCCGCGGTGCTGGTCCCAACAGAGAGGGCGCTGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-PBDA	103 A G ---			GCAGCCAGGAGCCGCTGCACCATGCCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGA/CTTG TCCTGCTCCGACCTAAGCGGAGAGCCCTCAAGAGCCGAGCCGAGGTGGG
EST12839 3	122 A G ---			CCCTCTCATGCCAGATGGAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAA/AGTCTCTACCCGCGAGCTTGCTCGCATACAG ACGGACAGTGTGGTGCAACATTGAAGCCCTCGTACC
ESTD-CTLA-4	48 A G ---			TGCAAAACACACAAAATCTTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTAAGTATCTAATGAACACAGCAGCTTACTCCAGAG/AGTCAAGTCCA AGGCCATTGGCTATCTCAACACTGGTGAAGTACTTGAAGTAAAGGAAACTTGAATGTTATTCAAC TGGATTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACITTAGCTTAG
ESTD-ACE	96 C T ---			ATGGCTTGCCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCT/AGJCCAGGACCTGGCCCTG CACTCTCCTGTTTTTCTCTCTTCATCCCTGTCTCTGCAAGCAATGCACGTGGCCAGCCCTGCTGT GGTACTGGCCAGCAGCGGATCGCCAGCTTGTGTGAGTATGCACTCCAGGCAAGCCAC
EST54419 8	88 A G ---			GATCAAGCAGTGCACACGGGTACGATGGACAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC/CTGTCTCCCTGCGTCGGGGGCCAACCCCGCTTCCA TGAGGCCATTGGGGACGTGCTGGCGCTCTCGGCTCTCCACTCTGAACATCTGCACAAAATCGGCCTGC CTTCTGCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCACTTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTAC/AGJATCCTGGGAGATGTAATTTGGGTTTAGCGTGGTCTGATGTTGTCTA CTATAGTCCAAGTGAA

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ESTD-PS-1	99 A G ---	---	---	GGGAGTAAACCTGGATTGGGAGATTTCATTTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAAACACAAACCATAGCCTAGJTTCGTAGCCATATTAATGGTTTGTGCCCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTCCAATCTCCATCACCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	---	GGCTGCCAGGGTTCGTTGGAGGGCCCTAGCGGGGCCCTGCTGGCGCTGGCGGTGCTGGCCACC GTGGAGGCAACCTGCTGTCTCGTGGCCATCGCCCTCTGGACTCCGAGACTCCAGACCATTGACCAA CGTGTCTGTGACTTGGCTGGCCGCGAGCCGACCTGGTGATGGGACTCTGGTGGTGCGCGCGGGCGCA CCTGGGCGC
WI-567b	48 A G ---	---	---	TCTCACACTGACCCCTTACCTTCACCTCCTGCTGGCTTGGTCTGAGCCCTCATCTCTTTTA CAGGATCCGCGCACAGCATCCCAACTGATCTGGCTTAGGCTCTCTCTCCATCCATCTCTCAAAAG GCTGCCACTGTGATCTTCCCAAAGGTGATCTGATGCTACCATCTTGCTTCAAGCC
WI-801c	58 G T ---	---	---	ATGGAACATTTCTTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTTG/JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGATGTTTGCAGGGGTGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCAACAGAGAGTTAA CATTCTGCCACCCCTC
WI-801b	58 G T ---	---	---	ATGGAACATTTCTTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTTG/JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGATGTTTGCAGGGGTGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCAACAGAGAGTTAA CATTCTGCCACCCCTC
WI-1099b	76 A G ---	---	---	GAAATTCACCTATACAAGAACTATTTCTCTAATTATTACATTAGTCTCATTTCTGAAATATTAT TTTTTACA/GJTACCCCTTGATTATTTTGTATTCATTTGTAAAGTCTACACAAATTAATAGTACGC TGTTTCATTGATAGTGTATCACAAATGTCTAAATACTTTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTGCTTTATGGTTTA
WI-2529	71 C T ---	---	---	AGGAAATGGCTGATCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA/C/TJCTTAACCTGCTGCCCTTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---	---	---	TAAGGGCCTGTCTTCCCCAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCCCTATAGGTAACTGAGGATGAAGGA GTGAGTCATATTGGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAGAGACTTTTACATTTTAGAC AGG/C/GJAGCAGAGCAGCAAAAGGAGAAAGGAAGT

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WI-2625	98 G A ---			GGG CAG T C C T G G C T G T A G T G G T A G A C A G C A C T G A A G G A T G G A G A A G A G A G A A A C A G G C A G A A G C A C T G T G G T A G T T A A C A A G G C T T A T T A G G A [G/A] C A A A T T G A T A C T C C C T G A G G A C T C G C A G A A A T T A C C A G C A G T G G A C A G G G T A T C T G T G G T G A A T T C A G T A T T C C A C T T G C A G G A G G A A A G C C A G C C A G C A A A G
WI-2924	54 G A TAGG	TGACCTTCCTA GTCCTCTCTTA	GCCTAAGTGT AATCAGAGG	TCTGTGTCAATATTCCTCTTTGACTCTGACCTTCCTAGTCTCTCTTATAGG[G/A]ACCCCTGTGATT ACACTTAGGGCCTACCTGGATTATTTAGAACAATC
WI-2939	72 G T GTGCCITT	GGCTTGCTCA	CTTGTGAGGG AAGGICTTG	CCATTGTGAGGTTGGTGGGTCACCTTGTCACTCCCTCGCACTCAACAAAGTGGCTTGTCTCAGTGC CTTT[G/T]CAAGACCTTCCCTCAACAAGAATGCTTTTCCATGCTCCCGTGTCTTTTGAAAAATTCGACT TTATCCTGA AAAACTCAGCTGCAGTGTATCTCCGGTATAAAGCCACTCCTG
WI-3203	99 G A AGACGAG	GGTATGCGGC	TCAAGTATTGC CTTGTGTGG	CTTGCTACCATGCAATTCACAGCATACAACCTCAGTGAATGCCGTAAACCCCATTTATAAAACAT CTTGCCATCGAAGGGTTATGCCGAGACGAG[G/A]CCACACAAGGAATACCTTGAAGTGACTTGGA GAATAAAGATTTTGGATGGATGAAGCAGAGAGGAGATGCTAAAAGTGA
WI-3473	101 A G GCCCTAGGGA	AAGCATTTTA GCCCTAGGGA	CCTGATGTCAC CAACATTTTCT	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTTGGGAGATAGTTGGTGATAGGCCCTGTTTGGGA GATTGCAGAGAAGGAAGCATTTTAGCCCTAGGGA[G/T]AGAAAAATGTTGGTGACATCAGGGCT ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCAATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTGGCTCCCC
WI-1796b	29 A G ---		---	ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCAATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTGGCTCCCC
WI-1796	29 A G ---		---	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCCTGCAGAGTAGGAAAGATGGGGTGAGT AGTCACATTAGGTATTTTCCAAATAA[C/T]AAAAATGCCCTCTGAAAAATATCTCTCCCATGTCCCCTGTC TAAATATAACATTTTCCC
WI-4360	93 C T AAATAA	GTAGTCACATT AGGTATTTTCC	GAGAGATATTT TTCAGAGGCAT TTT	GCTGAGCTTTGTGGCAGAGCCAGGGACAATTCAGCTGCCGGATTTTAAATAGATTCTGCAGCACTGCAA CAGGAACCAAAAATCAGTC[C/T]GGGTAACCTGAGAGTGGTTTTCACACCCAAA
WI-1959b	87 C T ---		---	GTTGTCCCTGTAGCAGACACAGAAGGCA[G/G]AGAGGAAAAAGCCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAATGCAAGATGAGCTAAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28 A G ---		---	CTTGAGTATCGTGGATTTGGTATACACAGAAATGGGAGAGCTGGAACATAATCCCCCATATACCA AGGGACAAAATGTATCTGTTTCTACAATTATACAGTAGGAGACATTATGTTCCATGACAATGGTAAT TTTTAA[C/T]GACAGTTTTTAATTGAGTGAAATACCATAAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTGCTATAAATAGC
WI-1980b	140 C T ---		---	

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WI-2015b	190 A G ---			TGTCAGATAGTCGCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAAATTATGCT ATATATTTATACAATATACAAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCACAAAGACTAT GTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACATGGTCTTTTCCAACTAGGTCATATACCTT CTAATACCATAGAG
WI-754b	49 C T ---			GAAGGCACAGGGAGAAGATGGCTGTCTATCTACCAGCCAGGGAGAGAAAGCCTACATTTATTGGTTAA TCCTATAAGTGCATCTTTAAAAATTGTATTACTTTAGA
WI-754	22 T C ---			GAAGGCACAGGGAGAAGATGGCTGTCTATCTACCAGCCAGGGAGAGAAAGCCTACATTTATTGGTTAA TCCTATAAGTGCATCTTTAAAAATTGTATTACTTTAGA
WIR-1b	56 A G ---			AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAAACTCTGATGTCGTACATCCAGGTCGCTG GAGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56 A G ---			AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAAACTCTGATGTCGTACATCCAGGTCGCTG GAGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-3b	72 A G ---			TAAATTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGTGAAGTCTAAAGTTATTAGCTCAGAGCCTCACACATTCACAGTACTGATAAACAATAAGCA AAGCTGGTGTCTGAGATAAGA
WIR-3a	69 A T ---			TAAATTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGTGAAGTCTAAAGTTATTAGCTCAGAGCCTCACACATTCACAGTACTGATAAACAATAAGCA AAGCTGGTGTCTGAGATAAGA
WIR-4	47 T ---			GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCCTGTCTCACACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGCC
WIR-5g	209 C ---			CGGGACAGAGAGACAGAGAGAGAGTTCGTCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGCCCTGTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACACAGG TTTTACGTCCAG
WIR-5f	196 C ---			CGGGACAGAGAGACAGAGAGAGAGTTCGTCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGCCCTGTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACACAGG TTTTACGTCCAG
WIR-5e	194 C ---			CGGGACAGAGAGACAGAGAGAGAGTTCGTCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGCCCTGTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACACAGG TTTTACGTCCAG

WIR-5d	191 A ---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5c	177 C ---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5b	159 A ---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAAGAGGTTATTAGGACTCAGTTCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTT AGGTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACAC AGTTTACGTCCAG
WIR-5a	37 A G ---	---	TAACCCGTAAACTTTGTCTTCCCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGAGCTCTGGGGTTGGGCGAG
WIR-6	63 A C ---	---	TTCTGACTATT[C]AAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-7	12 C T ---	---	GGCGTCCATGACTATCCTGGTCAATTGATTGACTAATGATTCTG[C]TGGCCCTTG
WIR-8	46 C T ---	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACATAAAGTTGTCAGAAGAGGATGA[C]GCTGAAG AAAGAAATTACTCTCTTTTGACCAATAAATACAATTGGGAAACACTGGAAACCCATGGCTTGATTACT GACAAC
WIR-2	56 C G ---	---	TGTCCTTGCTTATGCCTGCCCTCTTCGCTTGGCAGGATGATGCTGTCATTAGTATTTCACAAGAGTA GCTTCAGAGGGTAACCTTAACAGAGT[G]A]TCAGATCTATCTTGTCATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGAAGTACATAGCAGCATCTTTAACACAGCCGTGTGTTCAAAAT GTACAGTGGTCCCTTTTCAGAGTTGGACTTCTAGACTCACTGTTCTCACTC
WI-7069	93 A ---	---	GGTCATTTCCCTTTTATCTGTGAGGAGCCAGCTCTGACTT[A]TCTCTCTGTTCTGTCATCTCTCCC CCACATACCAACTCTTCCACCATGATGATTATACCAATAATACAGTTCCTTATAGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A T ---	---	CACACTGTTACACACCTATATTTCAAGTTTGGAAATGC[A/G]TATTTGCAAGCAGCAATACAAAAGTA TTTCATGAAGAATGCATAATCTCTGAAATTTATGAAACATCCCT
WI-18612	37 A G TGC	CCTATATTTCA AGTTTGGAAA	TTGTATTGCTG CTTGCAAT



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WI-18517	87	C T	CAGGAATCAG CAGCCTGA	TGTTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCCTCAACACCCCTCCATTTGTCAACCTCTACAGCCCTGCATGCC ACAGGAATCAGCAGCCTGAC/TTGGTGCACCTGTGTCACCAACACAACTGACTGC
WI-18668	76	C T	GGCGAAAAC TAGGCAAAA	GCTAAATTAAA CTGCACITTTT GC	CGATTGACAACCTTTTATTTTCAACTTAGGTACAGTCCAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAAAC/TTAGCAAAAAGTGCAGTTTAAATTTAGCAAAAGGCTCAAGACAGTATGTGGAAAGGAA GGTGAGATTTCCTCTCTACT
WI-18680	75	T C A	GCTGTCACTCT AGCATCTGGA	CCTCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT/CTGCTCGTTGTATATTCAGGAGGGGA
WI-18704	99	A C	GGTCTCCGA GGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTCTGTGCGAGCACACCAACAGGGCAGGTTGGGCTTGAAGGAGCC CTTGAGGAAACACGGGTTCTCCGAGGGGTAG/AC/CCAGCAGGGCTTCAGCTTAAAGTCG
WI-18673	29	A G	---	---	TGTGGCAAACTTGTTTTAAATTGCAAAAC/A/G/ACTTTAATTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAAACATATGAATATATAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T C	GTCGTGGGTG GGG	GCAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTATTTGGAGGTTAATTCCTATTAGGATATGAAAGGATTACAGCAACGATTGAGATT GTGTTCTCACGGAGGGCTCGGGCCAAAGTCGTGGGGTGGGGGTGCAGAGT/CJGTGTCCTCTTC AGTGGTATTTCGGACC
WI-18533b	91	T C	---	---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTTAAACTCCCGAGATTTCTTCTTTATTT TATATTTTCATTTTTCATCCTAAT/CJTACTGAAGCCATTTCTTTGGTTAACTTTAGA
WI-18533a	59	T G	---	---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTTAAACTCCCGAGATTTCTT/GJCTTTA TTTTATATTTTCATTTTTCATCCTAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A C	TCATCTGATAC CTGTTCAGAT TTC	AACCAGGATA AGGCTACAAC ATTT	GAGCATATGCTGTCATGAGGACCTTTCTATCTTACATTAAGGCTGGGAACTTACTCTTTCATCTGATA CTTGTTTCAGATTTTC/AAATAGTTGTAGCCTTATCCJGGTTTACAGATGTGAAACTTT
D49493	159	A T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGC	CAGGACTTGTGTGCACTGCAGACACAGAGCAGCATGCGGCAACATCACTGGGGCCAGAGAG AGCTGTCGCCAGTGCATCATAGGGGTCTTTTCATTTGCTAGTACTAGCCCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATT/A/TJGCCCTGGCCTGAAAGTGCCCATCATTCATACCCACTGTT CT
EST10030 7	98	T C	CATTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTTCATAGAGGAGACCTAGGAGGAGGTTGACACAGCACACTGCTCAGCAGATGACTTAAAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCTT/CJTATCCATACCACCACTGCTGATTG
EST10052 2	24	G A	GCTCACTTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG/A/GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGCCCTTC CTGTTGAGTCAATACCTGGTGGGAAGTCAATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGAGGAA A

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EST10605 2	118 C G ---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	GCTAAATTTTC AGAAAGAATT TTGTTT	CTTGGCTAAATCACAGTTCTGTATTATACAAAAAATTTGTTTTCTCTGACAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTAAATTTGTGGAGATGCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G ---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	GCTAAATTTTC AGAAAGAATT TTGTTT	CATGTGTCAATCCCATGATTGAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT/GJAA ACAAAATTTCTGAAAATTTAGCTTATGAATCATTAACACTGCAAAACAGAGAGGAGCAC
EST11260 8	101 G T ---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	GCTAAATTTTC AGAAAGAATT TTGTTT	TATGGAGGCCAGAGGAGTGACACTATATGTGGAAGTGTCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T ---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	GCTAAATTTTC AGAAAGAATT TTGTTT	TTTGATGGAGAAATCCGAGGCTGCCAGCATCCCCACCAGTAGATTCTTTGGACGAAGAAATCCT TCTGGGATTCAGCTTACCGCCCTTCCCTCATCTGCTGGT[C/T]TCTCCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G ---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	GCTAAATTTTC AGAAAGAATT TTGTTT	GAATTCCTGGGTATTAAATAGCGGGTGCCACAGGAGCACATAGGAAGAGCATCCAACCTACTTTGGAG CCCT[A/G]AGGAGTTTATAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGGAGGAAGGAGTGGAA
EST11772 6	74 A G ---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	GCTAAATTTTC AGAAAGAATT TTGTTT	CCAGGAATAAAGAAAAAAGAGTCAAGAGGAAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA[A/G]GACTATTTTCATCTGACTATAAGTGAATAAATACATTTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A ---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	GCTAAATTTTC AGAAAGAATT TTGTTT	CTTGCCATTATTTGTGCATGTTCTTAAAGGCTGTGAAAGATAACTTGGAAATGTGGGAAAC ACATAGATCCCAGA[G/A]ATTAAAGGGGCTGGAAAAGTAGCCCTTAAGAC
WI-16644	42 G A ---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	GCTAAATTTTC AGAAAGAATT TTGTTT	AGAGCAATGGTGCATCTCAATAAGCACTCATTTTGTATTAC[G/A]GGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAAGCCCTCCACAGAACTTCATGCACCCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGAT
EST12005 9	56 A G ---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	GCTAAATTTTC AGAAAGAATT TTGTTT	GCCTAGTAATCCAAAAGGAACATGTTTGTATATAACACTCAGTACAAAGTCTGT[A/G]ATCCAGG AAGTGACCAGCCCGACGCTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTGAATC
EST12055 9	32 T C ---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	GCTAAATTTTC AGAAAGAATT TTGTTT	GTGGAAAATTTTATCTGTTACGCTTTCC[C/G]ATTATATTTATCTTGTCTTGATTTCAGCACCC CACCCGATTGCGAGGAGCTTTCTAAACGTGCCCCTGTGAGCTGTAAAAAGTCTCT
EST12492 1b	95 A G ---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	GCTAAATTTTC AGAAAGAATT TTGTTT	CCCTAGCAAAATGACTTGGAGTTGTGTTCCAAATACCAAGTTACATCTGTTGCCAAAATTAAGCTCTC TTCCCAGAGGCATTAACTGAGATTAT[A/G]GGAAACGCACAGCAAAATGACGATGCAGCTTTTAA CCTTTTTA
EST12492 4	25 A G ---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	GCTAAATTTTC AGAAAGAATT TTGTTT	ATCTTGAGGTTTCTGGGCTGTGAG[A/G]AAGTGACATCTTTTACTTACCAGGTCAGGAACCCCTAT AAAGAACTGTGTAGAAAAGATATCAGGTCAGACTTTTAAAGGCTCTCTTATCAGCTCAATAAA

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EST12502 2	52 C G ---			ATAACTAGGGAGAAAACCAACTGGAGGCAAGTCCACAGGTCACACTGTCA(C/G)CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAATGCTCACGGGGGAAATGACCATTTTAAAGGGCCATGTG GTGTCGAGGCGAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAATAGAAATGATCGGTAAAAAGAAATAGGAATGCATATTTCAACTCACACTGTGCACAAA CAGGTGTTTATTATCCCAAATGACAGTGTGCCTGAGAT(C/G)CATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCTCATTTATTGTTCAAAACACTGTCAGTACCAACATGTCCACCGGGC(A /G)TTGAGAATACAATATTGAAGAAGAGTCACTGCCCTCTGGAAAAATCAGAGTATTGA
EST12817 9a	22 C A ---			TTGGGTTCTCCAGGATTCCAG(C/A)CTCGTAGCTGATGTGATGAGGTTCATCATCATGCTCCACGG GTCTTTGGGAGTGACCGGGATGGGAATCCATGTGCTTTGCGTACTCCATCAGGTCAITGGG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA(T/A)CAACAGCCCAAGTTATTTACCAGAAATTTGTTTGCCTTTCA ATGTAGTGTTAGCTTTAATACACTGCACITGTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGTCCTGT GGGTCTC	AGGATTCATGAGGCTTTAATCATAACCTAATAACTGTTAAAAAACACAC(A/G)TCTGTCACTTG CAGAGACCCACAGGGACACACATCTCTCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTGTGTTTCTTAAATGAAGCATAATAAACAGTTAAATCTCAGAAAAATCATCTATAGTTGA GTGTAAACTCCCTAAATCAGTCTTCTAGGGCCACA(C/T)GGAGCAGAAAGCAGCTTCCCCACCCAAAG CACCTCTGAAT
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCCCTTTAAAAATTTAATCGCTTTATACAATTGACACCAATAAAATGCAC(A /G)TATTTAAAGTTTACAATTTGAGAAGCTGACACGTGTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTCTTCC(C/T)AGCATATTCAGCTATAATCA CTTACATCCCTCCACAAATATTCCTGTGTGGCCAGGCCAGTCTCCTCAGTGTCCCATGAATAGCC AGTCTTATTTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTTGAGGAAATAAATTAATGAAATAGTCT GGCCATT(T/G)GACTAACAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAAG TCAGAGGAAACAAACATG
EST13230 6	72 A A GAGACGC	GCTCAGATGTG ACAGAGA	CCGGCTCCTGT ACAGAGA	GCATCATCAGGGCTTTTACTGAACCTTACAACCAACTTGGCGCTCAATATGCAGCTCAGATGTGAGAG ACGC(G/AT)CTCTGTACAGGCGGCTACTGTCTTCAATCCTTTGCATGCAAGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT	AACCAGATTT TGACAAAAA	ACAAGAGGTT TGACAAAAA	AAAGATATAAAACAACTCCCATCAGTAGCAATACAAAGTTATACATTTTAAACCAGATTTTCTCAGG CCT(T/C)TTTGGATACCTTTAGTAGTTAACTCTCTTTTGICAAACCCCTTTGTATATAACCA

EST13278 2a	51 A G	C T T C A C C G A A C A A T A T T T T A G	C A T A T T C T T G G G T G G T G A G A A	T T C G C A G A A C G T T T T A C A A G C T C C A A A C C T T T C A C C G A A C A A T A T T T T T A G G [A/G] A T T T G A A A T T A T T T C T G T A G T T C T C A C C A C C C A A G A A T A T G A C A G C T T G
EST13282 0	99 A T	C C A C A C A T T T C A G T C C A A G A	G A T G G A A A A T T T G A G G A A G G T T	T G C C T G A G A A T C C C A C A C A T T T C A G T C C A A G A [A/T] A A C C T T C C T C A A A T T T T C C A T C T C C C A T C A G A G G
EST13290 9		C A A T T T T T A G A A G T T T G G T T T	A A A T C A C T T C A T G G A A A T T T C A	A G C T A C T C G C A A G C A A T T T T T A G A A G T T T G G G T T T C T T [A/G] C T G A A A T T T C C A T G A A G T G A T T T T T T T C T G T G C T T A A C T T C A G T T A A G A C C T A A A G A C A A A G T G G T A T C A C A T C A C A T A T T T T G T A T G T G G G C T T T T T G
EST13518 2	45 C G		---	G A A C A T C C T C C A G T A T T G A G G T T A A A A T G A T T C A G C A T T T A [C/G] A C T T T A A A A A T T A C C T C A A T G T C C T G G A G T C G C A T A G T T T A A A A T G A C T T C T G C A C C T T C C T T A T A A C C T T G A T T G
EST13522 8a	66 A G		---	C A G G T T G G T G A T T C T C A A C T A G G A G C T A T T T T G C C C C C A T C C C C A C C G C A G T G T C T G G A G A C [A/ G] T T T G A T T G T C A C A A C T C G A G A G G T G G T G C T A C T G G A A T C A C T G G G T A G A G G C C A
EST13568 6	69 T C		---	C T T T A A G G A A G T G A C C A G A T G A A T C C A A T G A C C A A C C T G G T T G A G A G C C A T T G G T C T A G G A G T A G A A A [T/C] G C A C A C A A G G A A T A A G G G A G A A G G A G G T T C G G T T A G T T G A G G G A G A A A A G T T G G A A G C A T T T C A A G C T A A G T A A A T G G T
EST13785 0	101 C G		---	A A G A T T A C G G A C C A T A A G A A C T G C C C C C G A C C C A T A C A C A C A C A A T T T A T A G A C A G G T A A A A C C A A C T G A A A G G A A C A A A G T A A T G A C T T T C T T G A A C A A A [C/G] T G A T T A C G A A A G T G A A A G G C T A C A G G G T G A T T A C T A
EST14038 1	25 A G		---	C C T A A C C A T C T G T A A C C C G A G C C C [A/G] C A G T G A C C G G G A C T T G C T G C T T C C C C A T C C C A G C C C T C T C C T A T C A G C A T C C G C T A A G C G T C A G T C A G C A G G T G
EST14083 7	23 A G		---	C A A T G G T G T C C A T G T G A A C A T A T [A/G] A C C T A T T C A T A A A G T T A A A A A T A A T C C C T T C T T G C A A T C A C A G T G C A A A G G C A T G A G G G T G A A A G T C A T C T G C T A A A A T G A C C G A A C A G A G G A G G T A G G A G G
EST14221 5	42 T C	G C A T G C T A G A C A G A G G C A T T	G G A C A A G T C A A A A T A T T T T T A A A G A	A A T A C A A T G C A T T C T T T G G C A T G C T A G A C A G A G G C A T T A [T/C] T T T T G A A G A T C T T T T A A A A A T A T T T T G A C T T G T T C C C C C T C A C A C T A T T T T A A A T T G T
EST14812 2	50 A G A T A	C A A G T C A G C T T C T A C A T T C T G A	T A A A G A T T T A C T T A A A T C C C A T T A T G T A C T	T T C A C T T A G T A C C A A G G A T G C C T T T C A A G T C A G C T T C A C A T T C T G A A T A [A/G] A G T A C A T A A T G G G A T T T A A G T A A A T C T T T A G A A G T C C C G A G T T G C C T T T T C T A A C A T T T T C A T A T C A G G T G A A A A C A A T T T T T C A T A T G G G T G A T
EST14815 3	128 A T	C A T C A C C C A C C A T A C T G G T T	C G G G A A A A C A G T A C C G G A A	T T T G C T T C G G C A A T A C A T A G T G C G C A A T G C A G C G T G A G T T C G C G C C G T C T C C C A C T G A A C C A G T A A T T C A C C A G A C A A T G C G C A C C A C T T A A A T A A A C T T G C C C G T C A T C A C C C A C C A T A C T G G T T [A/T] T C C G G T A C T G T T T T C C C G T A

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EST15420 6	109	A	---	---	TTTAAACCCCAAGACCTTCTAGATGTCAGGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTTGTCATCAATAATCATATAGCCAAGGGACT[C/A]GGAATTTTGGCTGCTTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48	G	C	GGA	GTAACAGCAGCACTTTTATTAGACGTGAAAGACAAAGACAAACAGAGGA[G/C]AGCAGAGAAATAA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCCCTTGATCTGATGTAGTA
WI-16739	57	G	A	CACAAGC	AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGGTTTGCCATCACAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAAATGGCTCCCAAGGT
WI-16782	96	C	T	CACTGTAAGG	CTCTCCCTTCTAGACGTGGAATACACACGGATACAGTAICTGGAGATGTAGCAGCTGGCTTGAC CATAATGGTGGGAGTCTCACTGTAAGGA[C/T]GATGGAGGAACAGAAAGATAGAAGAGTTTGGGGT GCTGATGAAATTTGGGG
WI-16783	64	A	G	G	AAAAATGTAAACCTTAGAGGTTGCCTCTTTTGTGCACCTTTTCTTGAGATGCTTTTACCTGAG[A/G] CTAATAAGGATTGAACCAAGCAGATTTTTTAAATGGCAAAGTCCAGATGTAACCTCGAGT
EST15948 2	58	T	C	---	CAGGACTTAAGGTGCTTTTGCCTGGAAGACTTTAACTAAAGGTGAGGCAACATAGGAT[C/T]GTGA CAGCACCACTGGACCAAGGAGTGTGAAATGTCACACTAGCTGCCAGCCCTTTTTCCTGGC TGCTCTGCCTCCAGAGC
EST16088 8	89	G	C	---	GGTTTGAAGACGCAGCTTTATCTCCACCTGCCACTGGGATTCTCATTTTGAGAGCTGTTTGTGACGC TTTTCCAGAAAGGCCGCT[C/G]GGGTTTCTGAACCTCTATGGGCAITTTTAGAAT
EST16089 9	96	C	T	---	CGTCTGAAGTTTTCTTTTATCACAAGTCACATCAATCCCTCGGGCCCTGCTCAAAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCT[C/T]AAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24	C	G	---	ATCCAGCTGTGAAGGGACAGGAG[C/G]GTAAACACAGTCCATTATAAGGGGTGTCACATTCCTCA GGGGCTCCAAATAATGCAACATTTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83	A	G	---	TTCTTTTAAATAACCCACAGACACCCCATGACACTTCCAAATTTACAGAGCAAAAAAGTGATTGACAG CTGGTTCTCCAGGGA[G/T]TGGCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119	T	C	---	ATGGTAAACAAATCAGTTCAGGTTTTTCTGAGCAAAATGATCCCTTTGGTCTTCCCGTGGC CTCCTAAACAACTAAACAAACCCCTACGTCTAATCAGTCACCTAAGATAT[C/G]CAGGTGGCAAGT CTTTCACA
EST16118 0a	32	C	G	---	ATGGTAAACAAATCAGTTCAGGTTTTT[C/G]TGAACAAATGATCCCTTTGGTCTTCCCGTGGC ATGCTCTTAAACAACTAAACAAACCCCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA

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EST16151 2	53 C T ---			AGCCAATTCAAACGAACTCTATCAAAACACACAAAGGCGCTAGAGGAGAGATTAC/TAATGAACGT AAATAATTCAAGGCAATTTTGTATCTAAAGCATTTTGTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 G A ---			CATTGGTTGGGTAGGAAAGATAGTAGTGCAAAATAAAATGGTAAACACAGCAG/G/AJAATGGAA TTATAGCTTTCTTTTCATATAGGGAATTGAATTTATTACTGAGGTGATAGGCAGAAGTAGTA
EST16183 2b	59 A G ---			GCAGGTAACACTGTGGTTCAACACGTAATTGTTCTTTCATAAAGAAAGAAATATCTAGTTG/A/GJTAG AGGAAGGCACGTCTCTCTGGCCCTCTCTGTTTCATAATTTTATGTCACTGTCTTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ---			AATCTTAGGCTCTGGCTTTCAAAATCA/G/JTACAGACAGATAAGAGCTTTAAGTATTTTCGCATTT CCCCAGAGGAAAAGTCAGCATCATATAACCACATGGGTCACATGCTACGCACATGGTGTC
EST16229 2c	52 T C ---			TGTGAACCTCGAATTCGTTGTCCAAGTCTGAGTCACAGTTTCATTTGGGAGT/CJCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
EST16229 2b	45 T C ---			TGTGAACCTCGAATTCGTTGTCCAAGTCTGAGTCACAGTTTCATTTJTGGAAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
WI-16816	124 A G TGGGTTA	GGAGCCATTGT	GCCTAGATTTT	CAGACTTTTCTCACACCTCATTTGGCTGGAACCTGGGTGACATGCACATCCTTGAACATCATTTGGCAA AGGGAATGGTCAATCAAAATTTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGTTA/A/GJACTGTCC TGAACAAAATCTAGGCTC
EST16269 5b	49 G A ---			GCACACTCTCTGTGGCTTGCTCTGCCAGCTGCTGCCAGTGCCACAG/AJTGCTAGCCCTCATGG CAGAAGCATTTTAGCCAACTCTGGTCTGCTCCACTCTCTCTCTCCGCCGCTGGGGCTCACCACC TCTTCTCTCTCAATC
WI-16824b	83 G A ---			GTCACCCCGAGCCAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTAGCAGCGATAGTTTCCGGTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTG	CAGCTTCTGAC	GTCACCCCGAGCCAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGTT/CJGTTCTTATGAAGAAGTC AGAAAGCTGATAAACGTGGCTTACACCTTTAGCACGGATAGTTTCTGTGTTCCCAAGTGGGTGTGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ---			TTGCTTTTATTAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTCATTACAAA AATGGCTTCCAAACCAATAAAATGAAC/T/CJGGAATAAGAGCATAAAACGGAAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCACT	TATAATCCATCTCTCAACACACACACAAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTCAACAAGACCTGTGCTTCAAAATTTTCTCTGATAATGTGGAGAAATCTGCTCTTTATGTA

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WI-16879	79 C T	GATACAGGCC ATAATTTCCCA	CAAGGCTTCT AGAACTAGAGT CC	AGACAGGTCACAACTCCTAGGGATAAAGATATAAATCCAGACAGCATTATTTCCAGATACAG GCCATATTTCCCA[CT]ATAGGACTCTAGTTCTAGAAAGCCTTTGGGGAGAACAGGCCACCCAG
WI-16882	99 A G	GAAATGCGCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGTGGGAGAGACAATCTCCCTTTACCCCAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGTCTCTGAC[AG]GCGATTACCTGACATGTGTCATCTCCCT
WI-16888	70 G A	GCTAACTTTGG GCAGGTTC	AATGTTCTGAA TTGACCAAAAT TAA	GTAGTAAATGTTTCATCACTACCCGGGGAGAGCAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC[G/A]TTAAATTTGGTCAATTCAGAACATTCCTCAAT
WI-16905	75 C T	ACTGGCCTGT GTTGTTCA	GTCTACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTGGCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACCTTGGCCTGTG TTGTTCA[CT]CCCACTGCCTAGAGAGTATAGACA
WI-16910	74 G A	AAGAGTAAAG ATGGCGCTAG AA	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTCAGTATGTGCTTAAGGAGGTTATATTGCTATGACTTTTCATCTCAGAGAGTAAAGATGGCG CTAGAA[G/A]GTATCTGTATAGAAACGATACITTCATTTGGGCCTGAACCCAGTGAAGGT
WI-16918	93 C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAGAAAAATAAACTACCACCATTTCTCTGCTACCACAGAGCACATAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACCAGCAC[CT]GATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTCTCTGAAAG
WI-16947b	127 A C	GGAAGCAGA CCTGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCTTGAGCACAGGATT TGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGG[AC]CCA CGGCAATCAGATGAGATG
WI-16947a	58 C G	CATGGAATA GGCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCTTGAG[C/G]ACAGG ATTTGGCTGAGGCTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGGACCA CGGCAATCAGATGAGATG
WI-16966	43 T C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTACTTTAAATGCACACTACATAAACCACTAAT[CT]TAACTTGGTCCAACATTTT AGTATACTAATATGAGTTTATATACTGATAACTTGAATGCCATTAA
WI-16995	55 T C	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATTT CCAGCGGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAATAGTATT[CT]ACGGCTGG AAATCAACATGCCCTCTCTCTGTGAAGTTGTCAGCATGGAGCTGAGAAAGGCTGAGTCAATCT
WI-16992b	60 T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGT[G/A]CCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTTTGGGGTTAGGAA
WI-16992a	46 G A	AAGCACCAG AAGTACACTG TC	CACATTCCCTT ACAGTCCCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGT[G/A]CCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTTTGGGGTTAGGAA

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WI-17010	23	T C	T T C A C A G G A	A A T A A T A C G G T	A T G T T T C A C A G G A A A G C C A T G T C A T G A C A T T C A A A A C A C C G T A T T A T T A G A A G C T C A T T T A A T
EST171.27			A A G C C A T G	G T T T T G A A T G T	T G T T T A A T G C A G A C A A A A A T C A A G G C T A A C T A A A A G C A G A T C C A A T G A C C C A G T A C A A C C T A G A
9b	74	C T	C A C T C G G C A C	G G G A G G C A G G	G G T T C C C A C G
			A G A C A G A T	G G T G	A T T C G T C T C A A A C A G C A T C C C A G G C G G C A T C C C C C A C G G T C C C C A G G C T C C T A A G T A A C A A C T
			A A T T C T C T A T	G G A C T A T G G C T	C A G A G T C T T T G G G A G C C A T G G G C A C C C C T G C C C T C C C C A G G C T C C T A A G T A A C A A C T
WI-17040	94	T C A	C A T C T C A A G C C	T A T T C A G T G A T	C A C G C G T T C A T T A A A T T T G T A C A A A G C A T G A A C A C T C A G G A C A G A T T G G C A C A A T A C A T G C A G T T C
			A	G	G A G A A T T C T C T A T A C T C A G C A G T C A G C C A G T C A G C A G T C A G C C A G T A G T C C C A G T C T C G T C T T T T C C
			G C C A A G G G A T		A A A T C T T C T C A T A T T G T
			T A A C G T A T A G	G G G A T C C C C T	T T G T T T G T T T T T C T C C T C C C A A G G G A T T A A C G T A T A G G T G T T C T T A A A C A A G G G G A T C
WI-17044	47	G T	T G	T G T T A A G A	C C C C A C T A T A G T G A C A G C A G C T G C A A C C A C T G A C T C T C C T G C A G A A T G G C A G G A A T C G A A T
			T G G A C T T G T C A		C A A A A G A A A A A G C A A G T G
			G C C T A T A A C T	T G T A G A G T T A G	G C A T G T T G G A G C A G A T C C C A T G G T A A G C C A A A A G T G G A C T T G T C A G C C T A T A A C T A C T C T T A G
WI-17021	62	T A	A C T C	T G C A G C T G C	C A G C T G C C A C T A A C T C T A C A G G C A C A G T A A C T A C A C T T T A T A C A G G A G C A C A T G C C A A A G T G C C T G G
			C C A G A A A G G A		G A G T G C C A A T A A A A T C A A
WI-17065	90	T C	C T T	C C C A A G A G A C	T G T A A A A A A T G T A G A C A T G G G G A A A A A C A A T T C G T A A T C A A C A T G T G T T T T C T A C T T C C G G T A
			T G T A C A G C C A	A A T G A A A T C C T	C C A G A A A G G A A A A G C A T A A A C T T T C A G A T T T C A T T G T C T C T T G G G T
WI-17066	32	A C T	A C A T C A C T G T T	G A G A T G T T G A A	T T C A T A A G G T T G T A C A G C C A A C A T C A C T G T T T A C A G A A C A T T T T C A A C A T C T C A A A A A G A
				A	A A C T C T G C A C C C A T T A G C A G T C A T T C C C T G T A G C T T C C C T C A T A G G C A A T G G C A A C T G C T G A T C
					T G C T A C T G T C A T G A C T T A G T A A G G C C A T C A C A G G T T G C C A G A A C A T C T A C T C A A C T G T T C C A A G C A T
WI-17074	86	T G	---	---	A A C C T C C T A C A C A G G C C T T T G C T A C A T A G G A G T A T A T T T G G C C A A G A C T C A C C A C T A G A A G T G A T T
WI-17104b	108	T C	---	---	C A G A T G A G A A C T C A T G C T G G C T C A T C T G C A A G C T T C C T G A T G C T T T G C G A G C T T T C C C A T T C A T T C C A
					A A T C A G A A G C A G T C A G T G G C C C G T G G T T C C A G A C G G C T T C T C T C T T T G T T A A G A A A T T A
WI-17114a	37	T C	G A C T T T G T T T	T T G T A T T A A A	A G C G T C C A C A C A G A T G T T T C C A T C A A G G A C T T T G T T T T T C T C T C T C A C T C T G C T A T T T A A T A C
			G A T G A A A T T C	A T A G C A G A G T G	A A G C T A C C T C C C A A G G C C A G A T G C T C T A A G T G C T A A A A G A A G A C T G C A G C C C A C A A T C A G A G T T A C A T
			A G A T A G T C T T C	A A G A G A C	G G G A
WI-17150	76	T G	C T C T T	T T C T C A G A A T C	C G T G G C T G G A C T A A G T G C T C T T C C A T G T G G A C A C A T C T C C A C T G A A C A G G A T G A A A T T C A G A T A G T C
				G	T T C C T C T T T T G C A T A T C T C C A G G A T T C T G A A A G G C C C T C C T T T G T C T G C T C T A A T T T
			C A T T T C T T T G T		G A A A T C G A A T A C G T C C A T T T C T T T G T A A A A T A C A A T A A C G T T T A G A A G G C A A A A G C A A G A A T T C T G
			A A A A T A A C A A	C A G A A T C T T G C	T A A C C A A C A T T G G A A A G G G G A C A C A G G G A G G G C A G A G G G A A A G G C C A G A T T T T C A A C G G T T T
WI-17163	43	A G	T A A C G T T	T T T T G C C T T	C C T C C A C A T C T G C A G A C A A A



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WI-17178	127 T C	GGACTCCCTCA	CCCTCAATTTT	AGCAATGTCCCTCCCAATTTTCATTAGCTATGAGTATCAGTTTCATTTTCAGAGGGAATTACTGG
		GGAGGAGC	CAACTGCTTC	GGCGAGGGGGTTTAAATATCTGTGATGGGTTTAAATTCAGTGAGGACTCCCTCATGAGGAGGCT/CJAGAA
WI-17180b	81 C G	---	---	GCAGTTGAAAATTGAGGG
WI-17180a	47 T C	TGCA	TGCGACGAGAC	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACCTCCCAAGTCTCGTCGCACAG
		---	---	GGAGTC
		---	---	GCATTCACAAATTAC/CJGAACATCTTGCCCATTTTGTTTCATTATCCGACCCACACTGACAGATGAG
		---	---	GGAGTC
		---	---	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACCT/CJCCCAAGTCTCGTCGCA
		---	---	CAGGCTTCAACAATACCAACATCTTGCCCATTTTGTTTCATTATCCGACCCACACTGACAGATGAG
WI-17156	54 G C	TCCA	TGTGGG	GGAGTC
		---	---	TAATATCTTG
WI-17149b	79 T C	---	---	TGAGGTAGCAGGGCATCTTAAGAAATGTTCTCTAAACTTTAGATATCTCCCAT/CJTTCCACAGA
WI-17149a	48 C G	CAAGGTTGA	CCACGACGTC	ATCAATATATATTTCTTGTTGGAAATTTTAAATGTTCTTAACATATCTGCCTACCATCCACCTCAAT
		AGGAGGAACA	CATGA	TAATATCTTG
		---	---	CAGCGAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTCATGCACGTGCGTGGAA
		---	---	ACCCAATTGTCA/CJGTGTATGAACACTACAAAGGATGGGAAAGAACACATTTCTCTCACA
		---	---	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACAT/CJTCATGCACGTGCGTG
		---	---	GAAACCCAATTGTGATGTATGAACACTACAAAGGATGGGAAAGAACACATTTCTCTACA
WI-17197	67 G A	CTGGGGCTAC	GCATACC	ATTTTGCTATGTTGCTGGGCTGGACTCCAGCAATCTCTGCTGCTCAGCAGAGTAGTGGGGCTAC/CJ
		---	---	/AJGGTATGCACACCTCACCTGCTTATCAGTTTCGTTTAAAGAAATTTGACTTTTAGATGCGCA
		---	---	TGATTTTCAGTACTTTTCTCCCTTGTCCCTAGTTT/CJTAATTTCTCAGTGGACAAATGGACAA
		---	---	ACCACTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC
WI-17198	38 A C	CCTAGTTT	ACTGAGAAATT	TTC
EST18753	27 C T	GGTCTCAT	GGATCGCATGA	TCGCTATGCTACCCAGGCTGGTCTCAT/CJTCAGGCTCATGGGATCTCTGCTGCTGAGTGGCTGG
		---	---	GATAAGACACAACCTGCCACCCAGGCTGCCCTAGGAGTAGTCTTAATGCCCTGATGGTGGG
WI-17108b	74 C T	CA	CC	TTATTTTAAACATAACAGATGCACCTTGGTTTTTTACATCTCTGTTGCCATTCAGTCTCAAAGT
		---	---	AAACAC/CJGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACTTACAGAGT
EST19067	41 A G	---	---	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/CJGTGGCATTAAGTACATTTCAACT
		---	---	TTTTGAGCAACCCCGCCATCACCATTTCATCCATCTCCGT
EST19067		CGTGACCAATTT	AAAAGTTGAA	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/CJAGTGGCATTAAGTACATTTCAACT
2a	40 A C	TTC	OCA	TTTTGAGCAACCCCGCCATCACCATTTCATCCATCTCCGT
EST19125		---	---	CTGTTTCTCAGAGATGACACTGCCAACA/CJGTACAGATTTGCATACATAACAGTTATGTATTGGC
8	28 A G	---	---	TATTCACAAATTTACAGTAGTGTTTTCTCTCTGAAAAA

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EST20824 8	115	T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGAAGCCGGAGTTTATTATTATTCAAAATCAGTCTCTCTGAAAACCTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTGT/GJTCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50	A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCCAGATGGGGTCACATCCTCAGAACTTCTCAGCCT/GJGTAGCACAAGTGG ATGCTTGAAGAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGTGAGTGGGACCA
EST21904 b	128	G A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTT AGAAAGCAT	TGATTGTGGTCTGGGAGCAGGTGGGCAGTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTTCAATATGGCCATTTTAAATAGTG/GJA/T TGCTTTCTGAACACCTGCC
EST22111 3	82	T C	GAAGATCTGT CTGGCATTCCT	TGGAAAAACA GCCCCAC	CAAAACAATGTAGACATAAGGGAAACAATTCAGAGAGCTCAAGTCACCATGTTTGTAAAGAGAAGAT CTGCTGGCATTCCTT/GJGTGGGGCTGTTTTCCAAGGCACA
EST22197 2	78	T C	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGGGT	GTTTAAATGATCACTCACCAAAATCCACAGGAGAACTTTAAATGTTTACAAGCACCAATATTCTGCT ATTCCTGCCAT/GJACCGGCATCCTTCATGGTAGAGTATCACAAAGTAAAGTTTCTGGTTGTTTCAATC TACTTAAAAACCA
EST22311 9c	92	T C	---	---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATTCATGTTTACTCTAT/GJGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTCATCATCCAG
EST22311 9b	54	A G	---	---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG CAGTAGCATTCATGTTTACTCTATTTGCAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTCATCATCCAG
EST22311 9a	41	T C	GGATTAGATC ATCTTTTAT	TTGAATGCTAC TGTTTACAGTG G	TTTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATAT/CJACATAAAAAATCCACCACCTGTAAACAG CAGTAGCATTCATGTTTACTCTATTTGCAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTCATCATCCAG
EST22319	19	A C	---	---	TCGAGGAGCTCTGAGGAGC/GJACCAAGGGACGTGTGTCGCCAGGGCCACCGTGCAGGGCAAGTGTG GTCCAACTCCTTCCTCCCTTTACAAAACTCCAGCCTCACCCACACAAACACTGGCTGACAGGCCCTTCT TAAGCCTTTTTTAACGT
EST22433 c	103	A G	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAACTGACAGA	GATGTTAATGACITTCCTTTGAGATATGATGGAAAAATATTCAGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACC/GJCTGTGTCAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71	A G	AAATGGATCC TTATCTGCACA	AGTTTCAGTTT GCATGAATTTT	TATCCATTTCAAGAAAAAAAATGACITTAATAAAAAATACAAATTCATATCCAGAAAAATGGATCCTTATCTG CACA/GJCCAATTGAAGAAAAAAAATTCATGCAAACTGAAAACTATGCTTT

EST22993 5b	71 T C	ATCCTTTTGT TCTACCCCC	TTGCTGTAA TTTGAAGTAA TG	GCCTTTTATTGCTCCTTTTAAACATCAAATGTTTATAACACACATTTGATCCTTTTGTCTACCCCA ATTTC/CATTACAGTCAAATTACAGGCAATAATAGGCTAACAGAAATGCTTGCAATTT TTATTTCTCAGCTTACCAATTTGCTACTTATATCTCTGTACAAGGTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAAATTTTATTAATCTTTGCCTTT/AJATGGTTTGACAGTTTGCTCTTTCT T
EST23021 0	108 T A	---	---	ACAGAAATTTAAACATGCAAGTTTCATTTACATTTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTIG
WI-17387	55 C G	CCTTTGCAGAT TGAAGAAAA	GCCTTTGCCTA AGATTAATAGT AACTACT	TTTTTGGCTTGTCTGCAGAAATAGATGAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAAAGCTCCAGAGGCAG/A/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTCC TGTAAGC	AAAGGCTGTAGTTTGTGTTTGTGTTTCTTTTCTTT/GJATTGATGGGATTTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATGAGGCCCGAGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA
EST23733 9	31 T G	GGCTGTAGTT TTGTTTGTGTT	TGCACCTTAAA TCCCATCAAT	CTGACAGTCCCTGTGTGGGGGTGTCATGTGGGTGTGTGTGAGTGAGACATTTTACTGCGTCCC GTCCCGCCAGCCCTT/GJTGCGCCTGCTCACTGSCCTTGGTACATTTGTATTTCTGCTTGGTTGAAA TACCATCAGCCTTCC
WI-17470	83 A G	GTGTCCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTAACGAAATCTCACTACTGCAAAATGCATTGTGTCTCTAGCTAATGAATGCAIT/CJAGAGTATTG CCTGC/AAATAATAATTGAGATTCTATTTTAAAGAGCTTAGAACAGTACATGGTGCATAG
EST25356 3b	95 C G	---	---	TCCTTGATACAGGTAACCCAGTTTGTACATTTATTCAGAACTTCACTGTATCTTCAAGTTTGTAT CAGCATCTCTGTGGAGAAAGCAGTGTG/C/GJTATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26 A C	---	---	TCCTTGATACAGGTAACCCAGTTTGTACATTTATTCAGAACTTCACTGTATCTTCAAGTTTGTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCAACAACTT ACTACCAGTTATTGATAAT/CJGATAGAACCCCACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT ATTGCGCT	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCAACAACTT ACTACCAGTTATTGATAAT/CJGATAGAACCCCACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	ACTTCCCTGTG TAAACACTCC	CATTCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAGGCCCTACT TCCCTGTGTAACACTCC/CJGJATATTGTCGATTTCTAGCTATAAGAAATGGGGCCCACTAAGTGGGTC

WI-17623	46 T C ---			---	TGTGGTTTAAATTTCCCATATAATTAATGGTGGGCACATTTTC/GCATGTGCTTACTGGGTC ATTTCATATATCTTTGTGAAGCATCTGCTCCAATCTTTTGCCTGACTTTGGAGTTTITTTGGT
EST26419 1b	46 T C ---			---	ATTTCATACAGAGATACAAAGGCACTATGTGCAGTC/AJACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTTCATGATGGCTGTTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26419 1a	35 C A AG	ATACAAAGGC AACTATGTGC		CAAGAAGTTTG GACTGCCC	ATTTCATACAGAGATACAAAGGCACTATGTGCAGTC/AJACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTTCATGATGGCTGTTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26780 5	69 G C ---			---	TCAGCTTTAAATTTAAGGGACATGTAATAAAGATGCATTTGACAGGACAGCAGACTAGTTCAAGC AG(G/C)AGGTTAGACCAGTAACAACCAACCAAGAAAGCAAGTGTCTGTTTCCATCTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ---			---	TACTTCAGTTTAAAGGCAATTCACACAGAGACTGTCTC/A/G/GAGACGGGCACAGAACGACACACC GTAGAAACACACCACCACCATGCATGACGGGAAGCAGAG
EST27152 1	101 C T ---			---	CAAAGGATTTTATTTTGTCCCTAAAAAGTAAATCTAGAAAAATAGCAACCCACTGCAAGAAGAGTT CTATACTAAACATTTTCAATCATCTCTCTCTC/TCTTTCACATGGTGTACTCTTTCATGTACACAT CATCGGAACACAGACTGA
EST27504 0a	33 G A ATTT	GCATTTGCAA CAATTTAATA		GCTGGTGTGAT GCTACTGTAAAT G	TTTTTGCATTTGCAACAAATTAATAATTTATC/G/AJCATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGTCTTTCAGTATTTCTGTACACATCTGTTAACAAGAACCCCATACATT GGTAAATTCATCT
EST27662 4	51 C T CTCCAGTCTTG C	CACATTTCTGTT CTCCAGTCTTG C		TTATGAAATG GCTTATGTAAC	ATCTTAAAGGACCATTAGAAAAAGGCCAGTCACATTCCTGTTCCAGTCTTG/C/TJAGGTTACATAAG CCATTTCCATAAATTCATAGCCCTTCTTCTTAGAGTAACACACACTCTTGTITTAGGAATGTTTC
EST27788 3	100 A G ---			---	ATTTTATTAGCGGTACAAATTCCAAGGTGTAAGGGTAAAGGAAAGGCGAAGGCGAGGCAAAATACAT TATTGAGCTGAAAAACAACCTTTACATTCAGGGAC/A/G/GCTTCCAGACAAGCCCATGTAGAACCCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4	58 G A AGAACCCAC C	GGAAGTCATC AGAACCCAC C		GTGCAGAGAGG TACTCCAAGTA C	TCCTCTAAACTTTCCTTCTGTGTGGATCCCAGTGACGTGGAAGTCATCAGAACCCCACTG/AJGTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58 G A ACAATC	AATAAATTTTC AATCTGTCAAC		TCAAGAAGGCC TTATCCATTT	TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTCAACACAATC/G/AJAAATG GATAAGGCCCTCTTGACAAATTTCTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTAICTC
EST28036 4	37 T C ---			---	TCCCGCTTCCAAAAGCTTTATTGGCAAAATATGCTCTA/T/C/JAAAAGAATGATCAATCTGTGCTCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACCACCGCTGCTGAAGGAGAGACTGCTGTTGTG TCCACCCTCTATTTCATAG

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EST2483 7	31 T A	GGAGTAAAG GTGTTCTTCT TTAAA	TTTCTCGCATT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTCTTCTTTAAA[7/A]ATGGTATAAAAAATAAATGCGAGAAACATTAAAG GGAGATGTACAGACAACAGACAGACATGAGTTTGTCTGACTGTGACACACATTGGTGAAA AGAAATGGTCTAGTAATCGTTCCAGGATTTCCGGTATGGGCCCTCCCTGTCT[7/C]GGACACTGCCAACCC CACAGCTGGAGGGGCACCTTAAGGCACGTCATTTTGATTAGA
WI-17724	50 T C	TGGGOCCTOCC TGTC	TGGGTTGGCAG TGTC	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGCTATTAGTTACATCATACCAAGTGTACATACTG TT[7/C]CACATGATTTATGGCTGTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTC
WI-17730b	68 T C	---	---	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGCTATTAGTTACATCATACCAAGTGTACATACTG TT[7/C]CACATGATTTATGGCTGTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTC
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGCTATT[7/C]GTTACATCATACCAAGTGTACATA CTGTTACATGATTTATGGCTGTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTC
EST29041 5b	53 G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAAACACACATTAAGCATCATTTGTCACCT[7/G/A]GCTAACTCCT CAAAATCAACAATACCCCTTTATTTTAGCCATGAAAAAC
EST29128 4	58 A G	---	---	CTTTAGAAGGACACCAGTCTTGTGGACTTAGGGCTAACCTATTCCAGCAGGTGCC[7/A/G]TTATTT TCACITGGTTACGCTGTGAAGGACCGTTTCCAAATGAGGTTACAGTACACAGGTTCTGAGCAGACATGA GTTTGTGGGACACT
EST29912 3	103 C T	TCGCCAGCTT ACAGGCT	GCCTAAGTGTC TCATTCTCTG T	ATTATTAGGTATCTGCTGTTGGGGTGGGGTGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCT[7/C]ACAGAAAGAATGAGACACTTACGCCATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	---	---	TATTGGTATGCTTAGGGAAAGATTCTGATTTAGAGATAATTAATCTTAAAAAGTTAACTCACCATGAAA TTTAAACCTTCTGTAAGTGGCTTCACTGATGAGGCAGTAACTACATAGGGATAAA[7/G/C]AGCTCAGTA TCTGGAATCATGCTTCTG
EST30223 2	99 A G	---	---	AAATAAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATTTGAGTTACAAGCAA TCCAAATTACACTCTAAGTTATTTTAATATTC[7/A/G]GGAATTAATTTCTTCTAGTTCAATCTTGGGA GG
WI-16260b	86 G A	---	---	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCCAGA GTTTCACAATATAGGTAGGAGTAAACAGGCTCCTACCTTCCCTTCCGTTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAACTCTG GGT	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCCAGA AGAGTTTCAACAATATAGGTAGGAGTAAACAGGCTCCTACCTTCCCTTCCGTTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTGCTTCTTG[7/G/A]GCTGTTTCTTACCTACCCCAATATCATAGAAT GTTGTTGCTTCTATAATGTTGAGCTTCAAAATCTTTTGTCTTAATCAATCCAAATGAATTACCTGAAT TTCTCCTCTTGTTCAAA

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EST31951 4	87 C T	GGGTGTCCAG CCAACA	CCACCAAAAT CACCTCC	ACAGCCATTATTATGTTACTTGGTAATATCAGAGACTGAAACATTTTCACTCTTTTAGCAATGACA TCGGGTGTCCAGCCAACA/C/TGGAGGTGATTTGGTGGGAATTCCTATCACAAATTATCT
EST31968 8b	95 T G ---		---	CGAATTTGTCTCTCTATTATTTGTGATTCTAGTAATCCATAAAGATTGGGGGGGGTACTATAAGT GCATTTTATAATGGGATTTTCTGCTT/GJAAGTGGCCACTGATTCCTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST31968 8a	75 T C T	GCGGGTTACTA TAAGTGCAATTT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGTCTCTCTATTATTTGTGATTCTAGTAATCCATAAAGATTGGGGGGGGTACTATAAGT GCATTTT/CJATAATGGGATTTTCTGCTTAAC TGCCCACTGATTCCTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST32063 2	103 C T ---		---	TCCATGGATGAACAGACGCTACCATGCCACATCCCACTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGT/C/TGTTGAGGCCCATTGAAATAGCAAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G ---		---	AAGGCTTTCACAGCATTCAAAGGCACCTTGGGTGTTGTGCTCTAAGTTTCTGGTCACTGCAGCCCCC/A/G JTCTGATTAGGGAGCACCCCAAGCCAGTAACAATATGGTTC TTGCAG
WI-17800	29 C G	GGGAGCACAA GAGAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACT/C/GJAAGACTGGGATTAATTGTAGGAAATATTTACAG TTTCCACAAGTCAGAAGAGCTAATCCCAACCCCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34 T G C	CCTAAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCATTCTAAAGTCTGGGATGACTTTCCTT/GJATTCATCAATAGTAGAACCTAAGCCAAT TCAGAATCAGAATCCCTTTTGCCATCAAAATCCAGTAACTCCAAGCTGAATTAATGTTCATTCT GTATCTGATGTAGTTAACCATGGCCTGTCTCATGATTATATTGCTATAAGGAAGGGAACAAAATCTTTA TAGTGTCCAAAGATAATTAATTCCTGGTTTAAATCTTTGCCAGCAAAAGCAAAATA/T/A]CCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17860	121 T A	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	CAGCAACCTTTTGTGTTTATAGCCTACTTCTCAAAATTTGT/TATTTTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAACTACCA
WI-17866	43 A T	TTTATAGCCT ACTTCTCAA	CCGTTGTCAC AATCACACAA A	GAAAAAAGTCAAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCATGATC AATCGCCACGAGA/G/A]ACTGGATGCCAAAGAGTATGG
EST33301 4c	80 G A ---		---	GAAAAAAGTCAAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCAT[G/A] ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33301 4b	63 G A ---		---	
EST33460 1	44 G A CA	AGCGTGGTTTT CAATACTAAA	CTGTATTTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTCAGCGTGGTTTTCAATACTAAACA/G/A]GTAAACAATGCAANTATT TAACAATAATACAGTGATTAAATAAGCCATGGCATATCCAGTTGATGTAATACTTTTGCAA

WI-17904	50	A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACATAAAATGAACACAC/GTACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACACAAACACAAATGA
EST34149 5	69	A G A T	TGCCAAATAC TCAAGTGTGA AT	AACTACTAGCG AGAACAACTA ATAAAATC	GTCTTTCTTTGAGTGACACAAGCTTGTTCAATTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA TJAGTGATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95	C A	---	---	TGGGAAACATAAGTTAACTCAAGAATATATCCAGTCTTTATGTTACTAAACATTTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTC/AJTACAAAGATTAAAGAAAACCTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98	C T	GGACCATATG ATATATAACT CCTAAAGC	CAGAAATTATG TGATAATAACT CCTTCC	GGTACACAAATTTAATGGAAGGAACACAGGATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATACTCCTAAAGC/C/TJGGAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118	A C	---	---	CTCAGTAACCTCGGTGATAATCTGCCATTTATTGATTTATTATGATAAAACACCTCTCATTTGTA AAACAGCTAAGGTGACATCTCCAGACCCCAACCACTGTCCCTGTAATGTJAC/CJCTGCTGAGAGTCC ACATTTTGGAAATCCAAAT
WI-17996	84	A G	GTAGAGGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGGTGAAGCAGCATGAAACAAACATCTCCCAGGCCTCGCAGT AGAGCGAAGGGAACAG/A/GJGCTGCCCATGTGCCGTCTCTAAAGACGCCACCCTCAGGTTGATGT CACCTGTGGGAGACGGGT
WI-17136	33	C G	---	---	ATCTTTATAAAACACCATGTCCCTAAATGTJG/GJATTCACATATATGCACACCTTCOGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCT
WI-18041	24	A C	---	---	GCCACTGAAAAAAGGTGCTCTTCC/A/CJGTTTCTAACCTCCCTGGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAACTACTTAATCA
EST35164 8a	57	A G	CACAGCCCTGC OOC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTCAAGCACAGCCCTGCCCCQJAG/JCTTTGA GATTCAGAATCCAGAGGGTGTCTCAGTCCCTTGGTTTAGGTGCTTCTGTGACATTTCTCTTG
WI-18052b	67	A G	---	---	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCTTGGTTACACATCTTAGJ A/GJACAGCAGAGCTGCCCTGAGGGAGGGTTGTGTTTAAATGTCGTATGCATGCTCAGCACAGTGTCTGGC ATGGCCCATCCATGCTTT
WI-18052a	50	T C	CCTGAGTCTTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCTTGGTTACACATCTTT ATGGCCCATCCATGCTTT
WI-18054	46	G A	GGGAGTGGG GAGTAAAA	CGTCACCCCTGC TTCCA	CTGTTGTGCTGAGAACAGAAAGGGGTCAAGGGAGTGGGGAGTAAAJGATJGGAAGCAGGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGTGATTGTTGCTCAGGTTGTAGCAACAGAGGTAATG

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WI-18064	54 G A	GTAGTGCTA AGCTGTATTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAAACCTGTGGGTAGCTGCTAAGCTGTATTTTCAGAG[G/A]GAATGTCAC AATCATACCACTGGGGAGAAAGAGTAAGCACAGTGCTTATTAGTGCCAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97 T C A A	GCATAAAATT TCCAGTTGGT	CCCTCGGCACC TGCT	TTAGCACCAATTCTAGTGGAGCAGGATTTCTGATCATGGGGTGAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT[C/J]AGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C G T A T	AACCCACTAC TACTCAGAGT	AAAACTAATA AGAACTGGA GGTTTT	AAACCCACTACTACTCAGAGTGTGTAT[C/J]ATATTACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGATATTTCTGTACTCAGAACATTTTAGGTTGCAAGGATATAA
WI-18080c	80 C T	---	---	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATACTACTATGCCGTG TTTGACTTTTAT[C/J]TCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080b	65 G A	---	---	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATACTACTATGCC[G/ A]TGTGTGACITTTAICITCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080a	41 T C A G T C T C	GCAAATATCA ATATCAAACT	CAATTTACATA AGAGATAAAA GTCAAAACA	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCT[C/J]TGTAAATTAATACTACTATGC CGTGTGTGACITTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT GTGGGCATCCTATAAAAAGCAGCCATGTGTGAAACAAATGATATGCACAGAAAGCATCTT[C/G/A] TGGCTTGTACACGGGTTTCTTTCAAGAGGAAGATGATCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGGTTTGAA
WI-18086	63 G A	---	---	AACTACATAGTATGGTGGCTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGTACCTTTGGTATTCCT TT[C/C/J]TTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115b	71 C T	---	---	AACTACATAGTATGGTGGCTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGTACCTTTGGTATTCCT TT[C/J]CTTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115a	70 C T T	TTAGTGTACCT TTGGTATTCCT	AGAGGTCTGTC TTTCATACCAA A	TTTTGAGAAAGCACTCTGTAAGGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTTCTCTTTA GGTAAATTTGC[A/G]TAAGAACAAATAAAAGCATTTTAAAGTCCACTGCCGCCCTTAGAACT GGCAAAATATTTTACATCACACCTGGAATCTGCCCAAGCTTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAAGCAGCCATCTTTCCGGAAGCTC[A/G]TGGAGCACAAAGCAGA ACTCGGTGGGTAGAGTGA
WI-18136	78 A C	---	---	TGAAAGAGTCTGACACAGCGGACACT[G/A]TCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCTCGGAGACAGGGACAAAATCAAGAAATGAGCTGGAGACATTAATCCTGGCGA
WI-18169	115 A G A A G C T C	CCATCTTCCG	GAGTTCTGCTT GTGCTCCA	
WI-18190b	26 G A	---	---	



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WI-18190	62 G A	...	AAATATATAC AACACTCCCTT	CGTTTACCAT TTGTTAAGCTT TTG	TGAAGAAGTCGACACAGCGGACACTGTCTATAAGTGGAAACAAAGGATGAAGCTAAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGACATTAAATCCTGGCGA
WI-18181	100 A C	CAGATC	AGCAGAGTTC CTGCCCTC	CCTCCCTCTCT OCCCC	GACAGTGAACAACATTGAAACACAAATACAACAAAACATTAGGAACAAGAAATGTGTAAATCCAA TGTGTGAAAAATATATACAACTCCCTTCAGATC[A/C]CAAAAAGCTTAACAAATGGTAAACGTA TGTGTTCTTGAAC
WI-18215	78 G A	CTGCCCTC	TGGTGTGATT GTGATACACTT	CCTCCCTCTCT OCCCC	ATTACATAAAGCAATTCCTGAGTACAAACTAGGGGACAGGTATTTTACAAAAACAATAGAGCAGA GTTCCCTGCCCT[G/A]GTGTGCGGGGAGAGAGGGAGGATTTCAGCATTTTGGTGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60 T A A A	...	GGAAACTTG AGTTGAGATC	AAATAAAGGT TTTCAGGGGTT C	CATTTCCGAAATCTGATAGTTAAATATCCCGTCGGTGTGATTGTGTATACACTTAAG[T/A]GAA CCCTGAAACCTTTATTTTGAATTTGAAGTTTTCCTCAGAAACTGGGCAGAACTTTTCACATTCTG AC
WI-17892	76 T C A C A	...	GGAAACTTG AGTTGAGATC	CACAGAAGTG AATAGACTAGT GAGACA	TTTAAAAATGCTTAGATTTTCCCTCAGTATTTTATCAATAGTGTGTAAAGCTGGAAAACCTTGAGTTTGAG ATCACATA[T/C]CTGTCTCCTAC.TAGTCTATTAC.TTCTGTGGGCA.TTTCGGCAGAAAGTGGC
WI-18242	30 G A A A T C G T A A C A	...	CCCCAAATGTT AATCGTAACA	GCTAACACTTC TACTGTAACAG CTTTC	AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACCTTATCTCACCATTCCCTTCAAGCAAGTGAGGGTCAGAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119 C T	...	...	...	GCATCAGACATCACCCTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[CT]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C	...	...	...	GCATCAGACATCACCCTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T T T C A A A	...	AAATAGGAAA TAIGGACTATC	TTTATGCAICA TTTGIGCA	GCATCAGACATCACCCTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGCAAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G A A	...	GCTGTCAGCTA TTGTTATTCA	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTTGGATATGTTGTTTAGTGTCTATCATTAAATTTTGGAAAAGCTGCAGCTATTGTTATTC AAAT[A/G]TATCTTCTGCTCCCTTTTCTCCTTTTCTGGGATTCTCATTTCGCAATGTTTATA
WI-18330b	66 A G	...	...	...	AAACATCTACAGCTGTCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGGG[ A/G]TATGTAGGCAGTGAGTCAGGACTATGCAAAAACCTAATAAAAGAACATAATTTTGTGTTGAT TCACA

WI-18330a	49	G A A A G A	TCCTGTAAGA AATCAGGGAT	AGTCTGACTC ACTGCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATATAAAATAAAGAACATAATTTTTTTGTTGAT TCACA
EST37564 5	85	T C A G A	AAATTC AAGC CATCTACAAA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAATTC AAGCCATCTACAAAAGATTT[C]TCTCATTTGAGGCCCTCCATAGGCTGCAAAACACATCAAAAGGCAATTAC TGTACTGGAGAGGACTGAG
WI-18327	104	G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAGGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAAGCAGTACCTC CCAAACAATGGTGAACACAGCTTTGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATGCGGAGGCAGA GT
EST37624 6b	102	G A ---	---	---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACG[G/A]TTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
EST37624 6a	58	C T ---	---	---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGA TGGCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACGGTTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89	C G GCATCAA	CCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTTACCCTGCTGAGGTGGCCATGAAGCCAAAGCCCATGGAGAGACATTTTCAGA TAATCCAGCCCTTAGCATCAA[C/G]TCATCTTCAGTCTTTGAGTCCCTCCAGCCAGGTCCTCAAGCTT GTGGACACAGACAAAGCC
WI-18012g	117	A G ---	---	---	TTTTATCTGGGTCAGCTCCTTCTTAATGCCCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTTGGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGA[G/G]GTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	G A ---	---	---	TTTTATCTGGGTCAGCTCCTTCTTAATGCCCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTTGGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGA[G/G]GTGAAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C T CCCT	GCCACTTTTG CCCT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGGTCAGCTCCTTCTTAATGCCCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTTGGAAG AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T C ---	---	---	TTTTATCTGGGTCAGCTCCTTCTTAATGCCCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTTGGA AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGAAGTGTTCCTGATACA GCTGACGTTTCGAGGG
EST38390 4	75	A G CTCTGCATTG	GCAAAAAGGA CTGATTAAATAA	GCTAAAAGTCAG CTGATTAAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTACATGGCAAAAAGGACTC TGCAATTGTA[G/A]TTAAGTTTATTAAATCAGCTGACTTTAGCATTTGGAGATTATCTGGAT

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EST38512 7	91 T	TGACGATGCC AATACTTCG	CACTGCACTCT GGGAAGC	TAATAAAACTGACCCAAATTGGTAAACTGTCTCTGGACTGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACCTCGT/GJGCTTCCAGAGTGCAGTGATAACTGTTATAGCC
EST38519 0	24 C T T	CCTGCACCTCC TAAAGATCT	TCTGTTAGGAC TTGGGGA	CCTGCACCTCCTAAAGATCTTTT/CJTTCCCCCAAGTCTAACAGAAATGGTATATCTCTCTGGAAAA AGATGAACGTCATCAATGGATTGTGCTCTCTCGTTTCAGCTTTGATTTTTTTTGCTCTTGAGAACCTTG TCCTCCCTGCTGATTT
EST38575 1	66 T C A A	GAACATCCCA TGTTCTGTTT	AGGGAAGTA GTATAACACAT AAGAGA	AGTGGTCAAAATGTAATACTAATGGGGACACCAAGCCTCAGGAAGAACATCCCATGTTCTGTTTAA T/CJTCCTTATGTGTATACCTTCCCTTCTCTTCTTATACACATAGATTTTCCCTTAATTGCAGC CCA
EST38616 9	101 C G C T C	CCTGCTCCGOC	GAGGAATGGAT GGTBGC	CCATCTAGGAGGCTACCTGAGCTCTGTGCTCCAGAGTGGTGCTCAGGCCCGGGGGCCCGTGG AGTCTCCGGGGCCCGCCCTGCTCGCCCTT/CJ/GGCCACCATCCATTCCTCCAGGGG
EST38652 8	59 T C C A T T C A A	TCTGAACTGGG CATTTC A A	TTGCAAAAATG AAAGGAAAAA	TATAGTAGGTACTTTCTCTGCTGCAGCAGGAATTAATCAGTCTGAAGTGGGCATTTTCAA/T/CJGCGTG GTATTTTTTCTCTTTCATTTTGCAAGTAAAAAATCAT
EST38654 5	42 T C G T T T A C A	AATGGTCATTT TAAATATCA	CAGTGATGGTC CTTAATCTTCT ATC	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTTACATAT/CJAGATAGAAGATTAAGGACCAT CACTGAGGTCACATAGCTCAGAGGCAGATTAGATTGGACCCAGGAGGTTGGTTCAGCATATA GGATCCTCACTCACCTGGACAGCCTGAGAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCCG/WJAGGCCAGCGGGATGTGTGCCCTCTCTCCCAACTCATCTTTCAGGAACACGAGG ATTCCTGCTTCTTGGA A A
EST38707 9	75 A G ---	TGCTCCCTGA GGTGATAGG	TCACCATCGTG GACTTAAGG	TGACCTTGATTTCTTCACTAGAGGGGAGAAGAAATCACCTACCTTTTGGATGCTCCCACTCTACTTGT CTCCCTGAGGTGATAGG/WJGCTTAAGTCCAGCATGGTGACCTAAACTCAGTTTAAAAATTCTTGCC TAGCAGCACC
EST38775 1	40 T A C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATTCAA	GACTCTCAACCAAGAGAAAAATCAATAGGAGAGGATTGGCT/AJTTTGAATTCAGAGCAAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCCTCCAATGCCCTTTCATGAGTTAGGATCTCCTAAAGTGGTAC AAACAAACCAACATGGTGG
EST38815 4	91 C A C A	TGTTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTTTCACTTATGTGTGTTCAATCAACAAG TGTTTATGAGAACCCATTACACA/C/AJAAAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38858 4	98 C T T G A C	CACGAGTAAA AAGAAACTCA	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTGCTTACAACCTTCTCTCAAGTTTGGGGTGGTTCCATATTTGTTATTGTTATTATTA TTCAACACGAGTAAAGAAAGAACTCATGAC/CJ/TJTTCTCCTTGGACTCGCTCCTCTCCCCCAATCTCGAT ACCGACTGCACTGTG
EST38865 2	72 T C T G T G A T G C	GCTGTAGAATT TGTTGATGATG	GGAAGGACGG AGGACACAG	CCCTTAATGGATTTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAAATTTGTGCG ATGCT/CJCTGTGCTCTCGTCTCTCCCAAAATGAGCACATATGCAGGCGAGGCAAGAGCATGCTGGA TTTGTCTTAGTTGTTAA

EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCTAA	CCCTCAATAAA TCTCATGTCTCT CA	CCAATGAGAACCAAGTAATTAAACATCATTACTAGCCTAGACTCTAAAT/CJT/GAGGACATGAGATT ATTGAAGGGAAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTTGAAACATTTCCC TTATCAATGTGATCTCACACATCTTTATTTTATTTGTTTTCACTTTCTCAAAATATCGGATTGTGC TCATGAGAAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCA/GC/GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	---	---	TTATCAATGTGATCTCACACATCTTTATTTTATTTAT/CJT/GTTTTCACTTTCTCAAAATATCGGATTGT TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTTCTTTAT TTTT	CGATATTGAG AAAGTGAAAA CAA	TTATCAATGTGATCTCACACATCTTTATTTTATTTAT/CJT/GTTTTCACTTTCTCAAAATATCGGATTGT TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38909 5	47 A G	GCACAGCATG GCTAAAACG	GGTATTGTG ATCCCATCTT T	GCACTAAACTAACTTTTCATTGTGGATTGCACAGCATGGCTAAACG/A/GTAAAGATGGGAATCAA CAAATACCATTGAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT AACTGAATGGCAGTGAAAACACTACACATCAAACTTAGGGAATGTGTTAGTGTGTACGTTGAG GGAAACTTATAACCTCAC/A/GC/GCTTGTTCACAAAAACAGCAGACACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38911 9	85 A G	GTGAGGGAA ACTTATAACCT CAC	TGTTGTTTGT GAAACAAGCG	TAAACATTTCCCATTTGAATCCCTTGGTGGG/GC/GGGGGGGGGTGAGATTGCAGTGTCTCAAGATAAA TATCACAATATATCAAAAACTTCAAAATGTCTATGCAATTCACACACTGACATGAGCCACAAACATT CCTTTCACAGGCACTGTAC
EST38955 5	30 G C	TGAATCCCTT GGTGG	CACTGCAATCT CAOCCC	CCTGCTATGATGCCTGGGCAGATCCCGACCTTCGGTGAC/G/A/CAGGCTCCCTGCCAGGGCTGG CCCTTGACCGGGCTCCACAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39002 0	42 G A	GGACCTTCGG TGACC	CTGGCAGGGAG OCTG	CACGTGGCCCCTAAGTTCCGGGTCTCCTCAGTCTGGATGGCTGTGGAAAAAGCTTGGTGTGAAG GCCTAAGGAA/T/G/AGGGGCAGGGGGCGATGCCGCCAGCGAGATGGTCTGTGAAGCCTGTGGGTG AAAGACCTAACTTCTGGA
EST39004 8	79 T G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG OGGC	AAAGATAATGTATCATCACACGCAACATATAGAAACATAAAAGAAAAATAAGTATCCACCTTAAAT CCCTATTATTCATGATATTTTCA/T/C/AGCAACTAGTATATATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16398	90 T C	TCCCTATTATT CCATGATATT TCA	GAATGGTTGT GAAAAATATA TTGATAT	GGTTGCTTTCATGATTTTCTCATTTCTCATCAGGTTTCTGGTCTTGTCTCTCAATTTTAAACAT T/C/CTTTTATATAGGGAATTAGCCCTTAAACTGTGTACATGTGCCAAAAATTTCTCCAGTT
WI-16403	69 T C	CCTTGTCTC AATTTTAAAC ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGCTTTCATGATTTTCTCATTTCTCATCAGGTTTCTGGTCTTGTCTCTCAATTTTAAACAT T/C/CTTTTATATAGGGAATTAGCCCTTAAACTGTGTACATGTGCCAAAAATTTCTCCAGTT
WI-16406	24 C T	GCITTAATGGC TACAGAAAGA AGG	CCAGAACCAG ATGTGTTTAA AA	GCTTTAATGGCTACAGAAAGAAGG/C/T/GGGTTTTATTTTCTTTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTGCAATTTAGAGCAATAGGTGCCCTGAA

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EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTTCATGATTTGTTTCATCTGAGAAATAAACCTCCCTGCTCTAAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATACCTGGCAAATGAATGAGGTGCTC TTT
EST39294 4	63 G T	CCTGAAACAG GGATGCC	GCACAAATAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAACAGGGATGCC[G/T] TTCTCGTACTATGTTTAAATGTGCTGAGCCAGCAACCTCGAGTTACCCGGCCTTTACCCACAGCC AGCTCTGCTTGTCTGCAT
EST39366 2	72 T C	---	---	AGAAACATCTCTGTGATCAGAGGAAAGATGTATGTAGAAATCAGAAATCAGAAATCTGACTGAATTCCTAAA ATCTAT[C/J]ACACTGAGAGGAAATGGAAAGAAATGTTTGCATAAAAGCTTTTCCCTGACTCTCA GAGGGGTTCAGA
EST39371 9	86 A G	CATTGGATTA GGTGAGAGG	TGATTTGAGAC ATTTCACATTT TT	AAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTATGTGTGTAATCCCAGTTGAGCATTTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAATCAAATGCTTCTCTTCTAAAGATTA GACATTGCCCAACCTGC
WI-17177	23 A G	---	---	ACAAGTGACATATCCAAACCAAC[C/G]TCCATCCCCACCTGTGCCCTATTTCTTCTTGTTCTTT AGAGCCTTTTTCAGCTATTTCTGTGAAGCAACTGCACGAGGCCCTCCCCGTACTCCTCCCCCTGGAA G
EST39428 8	31 C T	GCTCCCCACA ATTGATT	GGTCCCTTATG AAGCCACC	AGGTCTCTGGTGTCTCCCAAAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCGCAAT TTCTGGTGGGCTTAGGTAATTTCTGTGCTTTTGTCCACAGAGCAACAATTAAGAAGATCAGGTCT GGCTGTGC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGTT	CAGGGGTGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAAATGAATGTT[C/WC]CATAACCCCGACCCCTGA CCCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGACTTCA GAGTAA	TCCTGGAAAC TGACATAAAC	AAAGCCCTGTAACTGAAGCTAGACAACGTCACCTTTGGAAAGAAATAACAGGAACCTATTTATAT ACGTAATCACCTTTTACCTGCTGCTACTGACATAGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCCC
EST39465 2	80 A G	AATGCAGGAG GGTGGC	CAATCTCGGC CCTCT	ATGGTGTCTATTAGAGGGCCACAGGGGATGGGGAGTAAAAAATAACATAAACGAACCTGAACAGAAA TGCAGGAGGGTGGC[A/G]AGAGGGGCCGAGATTGGGTGTTACGGGCAGAGAGGTGGAAAGACCAG
EST39501 0	81 A G	AAAGATTCT GTAGACATCT AACATTAG	CACCTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTCAGACATTTCTTGACCAAGCCATAAGATTCTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATGCAAGTGCAGTTCAAGTCAAAACCAATTC
WI-18387b	84 A C	---	---	CACAAATGGGACTGCTGAAGAGTGACAGTTGGACCTTACCTTTGGTGACCCCATACATTTGGTGCA CATGCTTTAGCCATA[C/J]CATGGTAACATTGACTATGGAGTCTTGGAAGGTAAATGTGGGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CCCTACTTTGG	GCTAAAGCATG	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACIAGTITTTGTG
EST40601		GTACCCCAT	TGACCACAAA	GTACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGTCTTGTGAAGTGTAAATGTGGGATG
9	78 A G	GCGTGGAACTT	TCTTGAAGA	GCTATGTAGACATAAGA
		GAAACAC	AAGCGTC	TCCCAGGATGGTTATTCAAAGCTGTGGACGGTGAACATTAAGACGAAAGAGGTGACTCGCGTGGA
		AGTGATCAC		ACCTGAACACIAGIACGCCCTTCTTCCAAAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32 A G	ATCTTCAGGAT	GCACACCCCTC	TCCATTGAGTGTATCACATCTTCAGGATAGGTA/GJATAACAGTGTGAAGGGTGTGCTCATTTTCTTC
		AGGT	ACACTGTTA	AGCTGTGAGTAGAGGAGTCTTCCCGAGAGTAGCAGTTGTGA
		CATTCTGGTCT	AAAACGTATTT	
EST43091	28 C T	TTATTTTGGGA	GTAAACATG	ATGTCATTCTGGTCTTTATTTTGGACA/CJGTAGCATGTTTTAACAAATCAGTTTTTCATAGGCAA
		CA	CTAC	CCTTTTGAACATCAAAAGAAATACAATATATTTTCAAAATTTCTCATCTGTAATTC
WI-18420c	108 T C	TTCCATTAAAC	AAATTCTCAGC	AGAGAGACAACAAGAAGAAATAGGGGAAATGGGAAGAACAGAGTGAAATTAAGCAAAATCTTGA
		AGGAAGTTTC	ATTGCTATAAG	TTCCAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAA/TTC/GCTTATAGCAATGCTGAGAA
		C	C	TTTCATAGGTACTTCATGGGA
WI-18420a	38 C T	GAATAAGGGA	CCAAGATTGC	AGAGAGACAACAAGAAGAAATAGGGGAAATGGGAAGAA/CJTAGAGTGAAATTAAGCAAAATCTT
		AAATGGGAAG	TTTAATTTTAC	GGATTGAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA
		AA	TC	TTTCATAGGTACTTCATGGGA
WI-18425b	101 T C	...	...	AGCTGATCAGCTGCTGTTACTGTGTTTTATGTGTGGCCACAGGAAG/CAAAAGATCAGACACCCCTGTC
		CACCTGTCT	CCTCCTGTGT	CTAGACAGATTCA/CJTGACACAACAACAGGAGGTGGGGTCAACAGGGCGGAGAGCCAAAGAC
		AGACAGATT	TGTTGCA	TAGGGC
WI-18425	81 A C	A		AGCTGATCAGCTGCTGTTACTGTGTTTTATGTGTGGCCACAGGAAG/CAAAAGATCAGACACCCCTGTC
				CTAGACAGATTCA/CJTGACACAACAACAGGAGGTGGGGTCAACAGGGCGGAGAGCCAAAGAC
				TAGGGC
				AAATTGAGGTCCGGTGGAACTATAAAAGGAAGAAAGAAAGAAAGTAATCAAGGGAGGCCAAAGTG
WI-18449	129 C T	CTTTTGGCTCT	CTCCCTGACT	GGAAGCTGATTGCTGATCTAACGTGCTGTCCAGTTCCCTTTCTTTGGCTCTAAGTGGGACTA/CJTC
		AAGTGGGACT	GTATCCAGA	TGGATACAGTCAGGGGAG
				ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTGGCCCAAGACATTATTTTATTTCTT
WI-18457	120 T C	...	...	AAATGTCCAATATCTGCTGATCTGTTGTGTTGTGACATTGGGGCCACAG/TTCJAAATAGGCTAAA
				AGGCAGTCCCACTGCT
				GGTGTATAGCTGCTGTATACCCACATGGCAGAGGTGA/GJTAGAAACCATCTCAAAGCCCTAAAA
WI-18462	39 A G	CCACAATGGC	TTTAGGCTTTG	TATTTACCATACATCCCTCAGCAAGAAAGTTTGTAACTCGGGTTTAGGGACTCCATTGAG
		AGAGGTGA	AGATGTTTCT	TGAGGACGTGTGACAAGCTCCAGCAGGGTGGGGCCGGCTGAGGGTGGGGTGGGAGG/CJGGT
		GGTGGGGTGC	GCACGATGGGA	CAC/TCCCATCTGTGCCCTGGCCGTCCCTCCACTCACCCACACCTGGCCAGTCCACGTTGAGGT
WI-18476	60 C T	GAGG	GTGACC	

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WI-18491	109	G A	AACAAATGGT AGTGGTATT AATACTATT	CGTGTGCATTT TCITGTAAATCC	CTAATGAGATGAATACATGGAAGGGGTTAGCACAGTGCCTAAACACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAACTATTATTAAATCCAGAAATGAC[G/A]GGATTACAAGAAAAATGCACA CGT
EST50757 b	79	C T	GAGCTCGAGG CTGCTTCT	ACCTTTCACCC GCCC	AGCCCCCTCCACTCCACTCTGCTTCCACAAGTCGGCTCCCGAGAGCTCGAGGGTCTCTTTTATAT GTGCAGGGGC[C/T]GGCGGGTGAAGGTCAGAGA
WI-17675	103	T C	GGACATTTGG ATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGGAAAGCACTAGAAACTAAACATCTTCACCAAGTGCTGAAGAAAAAGTGTCTTCGTTTTAAT TGCCAAGCAGGGATGTGGACATTTGGATGGTGACTT[C/T]CCTGGGTGGTTCCCCATAGATTCACCAT TGCTCTAATGGTGCTA
WI-16543	67	G T	AGATAAACTA CATTTGGGTTT	GATTCATCATT ACAGGGGACTT	GATCCATTACCTAGGGTAAATTCCTGAATGTCAAAACAAAGAGATAAACTACATTTGGTTTTGG[ G/T]AAGTCCCCTGTATGATGAATCAAGAAATCCCAAGTCTGCTTGCACCCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAGG TTGGGAA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAAACCATCTCCCCCTGACCCCCAGTCCATGGAAAAATGTGTC TTCCACAAAACCGTCCCTGGTGCCAAAAAGGTTGGGAA[C/G]TGCTGGTCCGTACAAAAAGTAATT G
WI-17690b	79	A G	AGGCAATTTTC TAGCTGTGTT	---	ACAACATGTGAAGAAGATATGTTGCTTTACTACAGTGGAGGATTTTCTAGCTGTGTTGATTT GGCTTCCCCTAT[G/G]ATTCAAGGACCCATAACTCTTGTTCACATCATCTGCTATGCTGCTG
WI-17690a	63	G A	AGGCAATTTTC TAGCTGTGTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAGAAGATATGTTGCTTTACTACAGTGGAGGCAATTTTCTAGCTGTGTT[G/A] TTTGGCTCCCTATAGATTCAGGACCCATAACTCTTGTTCACATCATCTGCTATGCTGCTG
EST51717 b	128	C T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAACTCAGTGTCACTCACTATCCAGATTT[C/T]TGAAGTGGAAACCCCTCCGACCC TGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTT[C/T]GAG CTGGATTATGCTCAAA
EST51717 a	39	C T	---	---	GATCCAACTCAGTGTCACTCACTATCCAGATTT[C/T]TGAAGTGGAAACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTTGAG CTGGATTATGCTCAAA
EST53012	97	C T	TGGTCACTTG GGGC	GGCTCTGCOCA GGC	TTTCCAGGTTGACAGGTTTATTCCACCCCTTCCATCCCATGGCCACCCAGGAGGAGGAGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGCC[C/T]GGCGTGGGCAAGAGCCCACTGGGTTTACATCTCTGT GGGCAGGTGTGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTCAACATT TT	AAACTGCAAATAACAAAACAAAGAGTCCAAAGAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCAACATGTAC[A/G]AAATGTGACAAAGATATCCAGATGTTTAA
EST53389	74	A G	GGAGACCTGC AGAACTTAA CA	GGCCTTTCTAA CAATAAATGCT C	TTTCGAAATGTCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGGAGACCTGCAGAACT TAAACAC[A/G]GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAAATAGGTTTTAACATGAAC ACATTAAGGGGAGATGGCC

[illegible]



[illegible]

TIGR- A003P30	117	C G ---			ACAAAGTTCAAAGGAGAACTTCCTTTGTTTAAATGCAGCTGTCCTCAGAAAGCCTGTGATTTCTTAGGA AACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTTAAAGCAGTGTCAC[C/G]ACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TIGR- A004S34	156	C T A			GCTTGCTTTTATGTTAGGTCGGGGGAAGGAGGCTGACAAACCGCAGACATCTGGACACCAGC AAGGGTCCAGGGGAGGTTGCAGAACTTCTTTGCTCTGGCTAACAGCTGTGATGTGACAATAGCCA AACCTCCTCATTCCTATAA[C/T]CTTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTT TACA TG
TIGR- A004T44b	97	A C ---			AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAGAGTCAGGAAGATAAACCCAAATGAT TGAGTATGATAAAGAAATTTTGCATGGCGATT[C/G]AAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004T44a	69	G A TGA			AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAGAGTCAGGAAGATAAACCCAAATGAT TGA[C/G]ATATGATAAAGAAATTTTGCATGGCGATTAAATAGAAAAACCTATAAATGTAGAA:AAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004V08	60	T C GGCATTCTCTT			CCTACAATCCTATAATATGCAAGGGTGGGAGGATGCAGGAACACAGGCATTCCTTAT[C/G]GCC TTTTGTGGGAAGGATCAATTGGTGCATGCACCTTAGGGGACAATTTGGGCAGTAGCTGTCAAAATTC AGTAGCTGTCAAAATTTCAAA
TIGR- A004V26	125	A G ---			TCTAGCTATAAGACCAGATTTTAAATATCTAGATATAGAATTATCCAGAAATAATCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA[A/G]AAGGT TTCAGTTTATAAATGCTTAAATACTGTATCTATTGCTTAAATACTGTATCTATTGG
TIGR- A004V28 a	29	A G CGATCTC			CCAGGCTATAATGTTGGGTGGGATCT[C/G]GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TTCCTCGCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCTAACTAATTTTGTG TATTTT TAGTAGAGACATTGTAATTTTAGTAGAGACAGG
TIGR- A004X20	25	T C G A			TAAGTTTTCCTTCTCTCTGTAGGA[C/G]GCTCCATGTTACAGTCAACTATAAACACATGGCTCATGT TCACCTCTGGGCTTCGCTTCAGAGGAGTTTGATATTTTGGAAAGTGGTACCTTTGTTCTGTGCTTTTCA GACCAACCCGCTCTTTCATTCTTCAAGGCTTCCTTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCCTT
TIGR- A004X30	26	T C CCAC			TTTTGAAATCTTAGAGTAGAACCCAC[C/T]GACTCTAGTAATACCTTGTAATAAATAAATAGTTTT AAACACTTCCATAAAGAAATTAGGGTGCCAGCTCCTTGATTTCCTCCCTAGGGATAAAGATAATCCAT GTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102	T G ATGCAAACT			CACGGTATATGCCTTATATATAGGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAAC[C/T]GTTGCTTTTCATGAAATTTCTAATTAAGG ACTGTGCTTCTTCATATTCAAITGGACATTATACAAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTAGTGATTTAAGACTG

TIGR- A004Z19	85 C	T	GAGCAACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGAGACAAGTTTATTGGAGGAGCTTGACACCCCTCTCTGCCCTAGCTTGAGAGAACAACTGC AGCATTTTCTCTTTTCTCTCCGATGACCACTTTTGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAAGGAACAGATC
TIGR- A004Z42c	89 C	T	TTGGGGGAGGT AGGAGACT	CAGGGCTGCCG GTCC	GTCTAGCAGAGGAGATAACTTTGAGGAGACAGCCCCAAGGCCAGGTAGCCTTCAGGGGGGGGCA GGGTTGGGGAGGTAGGAGACTCTGGACCGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTTC
TIGR- A005D17 c	81 T	C	---	---	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTCTGCTAGATCTCTTGGCTCTCTGTGCAGGATTCCTTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D17 b	79 G	C	GGGAAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTCTGCTAGATCTCTTGGCTCTCTGTGCAGGATTCCTTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D44	97 G	T	TTAACATTATT GAACCTTAAAA CTGTACAC	TTGTCTATTAT TTAAAGCCAAC AAAA	CATCAGTAACATATACACAAATTGGTCAATCAACTGAACCTTGCCTCCAATATATTTCTATACAATACTT AACATTATTGAACCTTAAACCTGTTACACTTGT/TTTGTGGCTTTAAATAATAGACAATGATTTTGT TCTATTACTTAGTGATAGACAAAGTGATTTGTTAGACAAGTGATTTGTTTAC
TIGR- A005E31b	27 G	A	---	---	GGAGTTCAAAATTTATAACAGGCCCTCTG/AJCTACAGCTGTACTGGCTAGGCAAGCTTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTGGCTGCTTGGCCCTACAAAGCCACCTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G	C	---	---	CTCAGTGTAAAAACTTTGTTTAGGGAAAAAATAAATCCAAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTGTGAGACAGAA/GACCCCTTGGGCTCCTTTATTIIGTCTTTTCAACAGGACC CCACAGATATTGGGGTATGTCATGAGGACTGGGGATGCTCTATTG/GC/GGATGCTCTCTATTT
TIGR- A005E42a	42 A	G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGGTTACTGCACCTTACAGAGI/GJCTCAATTTCCCTGATTTAGGA AGGCGATGCTAATGGGTATTGCATAGGTGTAAGTATAAAATGTTGTATTTAAGAGAAATCCCAAG CTTGGTATAAGGCAGAAAAATAAATGGTATAAGGCAGAAAAATAAATAG
TIGR- A005E46	76 A	G	CACCTGACTCG GTGCTTAC	CCCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGTCTAAGCACCTTACTGCGTATCAGGCACCTGACTCGG TGCTTTACI/GJITACATTACCTCACAGCCAGGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTG ACAC
U20979	24 C	T	GCAGGGGTGA CGTATGTAGA T	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAAI/CTGCTTAGGGTGTCTCCCCACAGACAGACATACTTGAACCG ACTCAATCTCTGTGTAAAGAGCACTTTGTCTGCTTACGGACCTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTCTCTTTGATATTTGTAAAAATTTCCCAAGAGCCGCATATGAATCTGCC

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X57830	106 GC CT	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTGAAAAAATAATGAGATTGGA AAAAATTAGACAAGTCTAGTGAACCAACGATCATATCTG/CJ/TATGCCTCATTTTATCTGTCAAT GAAAGCGGGTTCAATGCTACAAAATGTGTCTTGAAAAATGTTCTGACAGCATTTTCAGCTGTGAG CTTC
X74070b	72 T G	CTTTTAAGAA ATTTTGTTTA TGGATC	GGGCTTAAAAA TATTAGAGATC TAGATT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTATATATATGACTGCTTTTAAAGAAATTTTGTATTG GATCT/GJGATAAAATCTAGATCTCTAATATTTTAAAGCCCAAGCCCTTGGACACTGCAGCTCTTTT CAGTTTTTGTCTTATACAAATTCATTTTGCAGCTAATTAAGCCGAAGAGCCCTGGGAATCAAGTTT GAA
Z48804	44 CT ---		---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTCTCTCATCACAG/CJ/TTAGAGCTTCTTCCCGAAGGG CCTTTAGGATAGGAGAAAGGTTTCATGCACACACGTGTGAGAAATGGAAGAGCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTGGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGAAGG TCCA
D28513b	133 A G ---		---	ATGACCAAGCCACCACATTTAGAATTTGGCTGCCCTTGGAAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTTTGTATTGACTGCATGAATGC/A GJTGCGGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85 A G ---		---	CCACTCCATCCTGATGCCCAAGTTATCCACAGCCTCCTTCCCGACCAAGACCCCTATCCACCTGGACC TCCATTTTCCCTGTAA/JG/JTTCTCCAACCTGATCCTACCCCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAGACACCACTACCCCTTGTAACCTACTGCTTCTGTAC
D29833a	21 A G ---		---	CCACTCCATCCTGATGCCCA/JG/JTTATCCACAGCCTCCTTCCCGACCAAGACCCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATTTCTCCAACCTGATCCTACCCCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAGACACCACTACCCCTTGTAACCTACTGCTTCTGTAC
D31762	82 G A ---		---	CTCCCTGCCTCCTCCTCCTGCTGATGCTCCGCTCAACAGCCGAAACCTGCTTGGCAATGGGGG GAGGGGCGTTTC/GA/JCTTTTCTCTCTTGCGCTTCTCTTATTTCCACAACCACTTCTCAATAAA GCCAAAATCTTCTCTTCTCCCTCAGGCCACCTCCTGCTCCTCCTGCTGCTGGCTTTT CTGGA
D37931	64 T C ---		---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTGT/CJ CCCAGGCTCTGCTCCTCAGCTCATTTCCCTACTCTTTTCTCTATATAACTCATTTCTATTAATACATT GCACCAAGAGATATGGAGACATAAACCTGTAATGAATGAGGCTGGGCTTTTCTGTATAAAGCTTCC TTT

D63807	101 C T ---	---	---	CAGGAGGACTTCAGTGCAGTATCCCTGCCCTTCAGTCTCTTTAGAAATCAGATCTGTGTTCAATCC ATTGTTAGAGGGAGTGATTTTCTGTCCAC/C/TAAGAGGAGACTTTTGTTCACAAATGGATCAC AATGCAGAGGAGTGTCTCTCCCGCTCGGCTTCGGTGGAGGGTGACCTGTGCCAGATGAC
D90145	21 T C ---	---	---	TGGGAACATGCGTGTGACCTC/C/JACAGCTACCTCTCTATGGACTGGTTATGCCAAACAGCCACA CTGTGGAGCTCTCTTAACCTAAATTTAAATTTATATACATTTAGTATTTTATAATTTATTTTGTAT TTCACAGTGTGTTGTGATTTGTCTGTGAGAGTTCCTCCCTGTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
EST14035 1a	59 T C ---	---	---	ATTATCACTCTCAAAAATTTGGTGTGTGTGTTAAAGTACTTCTTATTATGAGCCCCC/T/C/JAGGGA CCAGACATGTTATTATCAAGCCCCCTTATATACCATCTAAT
EST16668 5	71 C T ---	---	---	GCATTTTAAAATTCACATTTGAATCATTATTTACTATTTATGATGTTTACATAACAATTCAGTATCATT ATG/C/T/TGTAGATTTTCAGATGTAGGTCTGTCATCACTGAGCACTTATCT
EST16904 7	57 C T ---	---	---	ACAGACTATCGCCAACTTATAATGCTTAACTTTTATGATCAATAGTAATAAATTAC/C/T/JGAGATA TTCACACTTTATTATAAATAGGGTTTGTGTAGATGATTTTCCCACTGTAGGTTAACAT
EST21863 9	49 A G ---	---	---	TTTTAAGTACCAGGCACTGCTGGAACAGGATGAAACTGTACACCC/C/G/JTTACTACTTACTC TTCACCTCTTCAACTGATCCCTTAAGACTTCTACTTAGCAAA
EST21885 6	80 G A ---	---	---	GGCTGTAAGTAGAATCAAAGGTTAAGAACATTTTATGCACCTTATTCACAAAACATTTACTGAGCATA CTAGGTGCTGGG/C/G/JGTGACAGTGAGCAACAAAACACAA
EST22623 8a	26 A G ---	---	---	ATTTTAGTGCAATGACAAAGCCCCAA/C/JAGAACAGAGGATCAAAATAGATTGAAATGTATTACC TTCATATAAGTATACGAAGTTTAAACACAAGTATGGGAGT
EST22644 2	98 A G ---	---	---	AAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTTAAACAGCACTAAAAATAA AAATTTTAAAATGATTATCCATTATTTACAG/C/G/JAAATGTGGAAGATGGCTTTTAAACCC
EST23587 1	31 T A ---	---	---	CCCTCATTTATTTAAAAGACGGACATAAAAAT/T/ATATACAACAAAAACCCCAAGTCACATTTTCAG GAGGTAAAACCTAAAAGTCTGATATGAAAATATGGTGG
EST24246 7	106 T C ---	---	---	AAAGATCTGGCATTATTCACATCATTTCTAAATATTTTGTAAATTTTCCATGAGTATTTTTTCA TGCCCAAGCATTTTAACTATCATTTTACGCTAAATACC/T/C/JGAATAACCCATAGTTACAGAATTGG GTCTGTGTAACCTCAAT
EST24308 3	45 A G ---	---	---	TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT/C/J/CAITTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24435 6	73 G A ---	---	---	CTTGAACCTCTGGCTCAAGTGGTACGTCGCTCAACCTCCCAAAATGATCGGATTACAGGCATAAG CAGCC/C/G/JTGCCTGACCCACATTTCTTTATCCGATCTGTTGATGGACATTCAGGTTGTTTC
EST25089 6	25 T C ---	---	---	TATTGTGCAATTATCAAAATGGTTA/T/C/JAGTTTTCAAATTTAAACCTGTAATGATTCTCTATGTATAAA ACAGCTTTGAAGTGTAAATGTAGTTTCCAAATCGTTAGTTAATGCTACATT

EST25476 9	33 G A ---	---	AATGATCTTTATTTTCAGACCTGCTCCTAAA[G/A]C]TTCTCCTCCTCCTTAAACCAACACACA AGAGGTCCTCTTGCTGCTTTCATGGACTGGCGGCTGGGACTTGGACCGCTGCTGA
EST26183 2	70 T A ---	---	AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACCTTTGTAAGATTGATCTCTAAATAAG ATTTA]ACATCTCTGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28 T C ---	---	AGAAAAAAGGTGCTACCGAACTCATGTC]GATAGCGCTTCTTTAGGCACATATTATAGCATT CAGATGAAAGTTCTGTAATCACACACACACTGTGCCTCTAACAAACACGGTGACTCTGA
EST27816 5a	26 T C ---	---	CAACTCAAGGTACAAGACAATTGCATTC]TAACATTGTTATAATAAAGGAACATCAGATCAAT CATTAAAGGCTCCAGAGTGAACAGCATCTTCATAACCTTCCATGTT
EST28588 0	78 A T ---	---	GTTTAATTGGCGTATGGTCCACAGGCTGACAGAAAGCATGATGGCTTCTGGGAGGCTCAGGAA ACTTACAATCA]T]GGTAGAAGGCAAAAGAGAGCAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGAT
EST30226 5	25 A C ---	---	TACTCACACCGACATACATATCTCA]C]GTAGAATTAGCTATAGCTATGCTAATACTTCACTTCTTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAACAAGACAGACTCATTTCCCTTTGA G
EST30935 9a	59 C G ---	---	AGCTATGGTAGAGCAAAATCCAGTGGTAAATCAAGAACTCTAAAGTTCAAGTAGAGA[C/G]AGGT GTTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7	25 G A ---	---	CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCCCTCTAAACCTGTGTAATAGAATAATGGCCAAAT ATTACAGTTTCTCACCTTCTCTATGAATACTGGCACGTGTTTATTTTCATGTTTATGTGAGTTTCTATGC ATAAAAATCCCAGTAAGA
EST33274 4	27 T C ---	---	TGCTTTGTTCCCTCCAAATCCTAAAATTC]GTGTGCTTCAAAGAAAITCGTGGAAGGACTTTGAA TACGAGTTTGTACCATAATCAAGTATCTTGAATACAGGTTTCAGATAACTATGGAGATGATACCATI GGACTAGGTA
EST33352 7b	75 C G ---	---	TACACATTATCAAGAGACCACCTGACATGCATCTCCTCCGAGAAATACATTGTCCTCTCTAGAGA AGTTTAA[C/G]GCACATAGTATTTTACTAAGAGAAATATCTCTTGGTGTCATATCTAGGGG
EST33424 1	126 A C ---	---	ATTTTCCCACAGCAGAGTATTTTATTTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAAATGTTCCACAAAGATTTACAATCTCAGTCAATACACACTGAGCAAC[AV]AAA CAAAGGTGTGATCCTCTT
EST33488 7	90 A G ---	---	CCTTTGGGGGAGTTTAAAGCCAGAAATGTGACAAAGTCACTTACAGGAAGACTGGAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[AV]G]ACCATTTCCCGTCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST33508 1b	45 C T ---	---	AAAAACATGCTATTGAACAAACCTTTTATAAAGAATAAGTTGA[C/T]TGAAAAAGCAGTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36 A G ---	---	AAAAACATGCTATTGAAACAAAACCTTTTATATAAGAA/GJTAAGTTGACTGAAAGCAGTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---	---	ACAACATAGGACTGGTTATCTTGTTTTGAAAAAATATGTTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAA/CJ/TJCTTTGAACTACAGCCTGAATCCCCC
EST34739 3	97 T A ---	---	GAAATATCCTTCCCAGTGGCAGGAAGTGAAGACTCCAGATCAACAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGGAACCTC/T/AJGGTGCCTTACAACCTCACTACTGCAGAAATTCCT TGTTGTGCCTCATAAACA
EST34792 6b	104 A G ---	---	ACCTGACTGCTTTAAAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCTCCTCAGGATGTTCCCTGA/A/GJGATTACAGGAATTCCTTAGTCTATTACA AAGATTTTGTGCTGTG
EST34835 9b	93 T G ---	---	GGAATATGTTCCCTTTGCAACAAAGGTACGTTTATTCGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGICTATGTTGCTTTCTCGT/GJGGCCTTAAAGAAACAGACAAATTTGTCTAAAGAT
EST34835 9a	82 G A ---	---	GGAATATGTTCCCTTTGCAACAAAGGTACGTTTATTCGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGICTATGTT/GAJTGCTTTCTGGTGGCCTTAAAGAAACAGACAAATTTGTCTAAAGAT
EST35230 0	93 G T ---	---	CACAAAGGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAGAGGTTCTC/GJGCCCTTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---	---	TCCTTTCAAATTTTGTAGTAGGCATTTAATG/C/TJATAAAATTCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTTGGGCATGTTGTTTCCATTTTACTTAGTTCAGAACTTTTCAATTTTCATCT
EST35708 9	32 C T ---	---	CTGCCCCAAATTAACCTTTAGGCAAAATGGAA/C/TJAGACTTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTTCCCTCTCTGAGGTGGCACCTTTCCCTGTTGTG ATGTGCAAGTGIGGCT
EST35747 9	51 C G ---	---	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA/C/GJATGTTAAACGT TTCCCACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCTTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---	---	TGGTCCATTATATAAACTGAGGGAACAAACGGTGCTGACATGGCAGACATTTATTTCAATGGAGA AGTTCCCTCCCATGAAACCAAGA/C/AJCTTGCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAGGCCTGTGA
EST36301 4	93 C T ---	---	CACCTGTTCAATGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTCTCAGCCTACAGC AGTCAGGAGGCGAGCCATGGCCCTG/C/TJGCTGATGGAGCTTGTAATTTAGCCCCAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33 G T ---	---	GCCATCAGCCCCACAAAGACATGACTACCAACGC/G/TJGGCCCCCTTGACCCCTACTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGGCTTAGTCGT

EST36620 6	50 G A ---				GACITTTATTAGATAAGGGTTTCGGCTACCCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTTAAATATGGGAAATAAAATACAAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 C G ---				CCTGTGATGTGCATGGTGCCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCACGTATGTCAGGA AAGGAACTCTGGGATTCTCTA[C/G]AGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTTCA
EST36729 9	62 C T ---				GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCCTCTCTCTAATATCTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACCTTAGCTACCCCTGGACAATGCTATCAAGTGTCTGGGAAAGGGAG
EST36823 6	103 A T ---				ACTGCTGGCCGATGATTGGAGCTTGAAA-AACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATT[A/T]TCTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---				ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAAACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGATGCAGTTT[C/G]TTA GGGAATTAAGACAATGCAG
EST37054 3	88 T C ---				GGTCTACTCTCTGCCAGGACGGTTTGAACCTCTGAGCTCAAGTGACCCCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACACACCTGGTCTTGTTTAAAGTAACCACTGAA C
EST37269 3b	105 T G ---				AATAGTCTATGGTACGGGCCCGTGGGATGTTAAAAATTGGGATTTTAAATTAGATTGGAACATG CAAAACCAGCAAAATTTCTCAGCTTATATTTTGAAGTC[T/G]CAGGAGAAAAATGGGGTCC
EST37284 2	93 G T ---				AAAAGACCTTTCTCAAGCAGTAAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCCAGAA GCTCTCTGGATAATGTCACCTCTAGGA[T/G]TAAACACAGGTGTTAAACCCCTGAGATAGCAACCCT CTTGGCTTGTGAGGAATA
EST37315 2a	90 A G ---				AGATGGGGTCTTGTAGCTTGTCTGGGCTGAACATAAGATATCTCTCTGCTCAGCCTCCAGGTTAGT TGGAACATATAGTAGGAGTATC[T/G]CCCTGCCCTGCTAGAACTTCAAGTTTGTATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---				CCTGCCATGATAATGTTAAACATATCAAGATCTCTCTCAAACTT[C/T]AAGGGTGAAAAGCATACC ATTCCATTTTGTGAAATATCTTCCATAGCCACACACATTTTTCAGGCACCTCTAGCTACTACA CGA
EST37376 8b	101 G C ---				GTGACATCATGCTCTTCAATGCCCTTTCAATTAAATAGTAGTTGAGCGCTGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGTGTCTCTGCA[G/C]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGTCAGG
EST37376 8a	41 T C ---				GTGACATCATGCTCTTCAATGCCCTTTCAATTAAATAGTAGT[T/C]TGAGCGCTGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGTGTCTCTGAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG



EST37378 9	63 T G ---			ACACACAAAAAATGGTGGCAGAAAAATCTGGAAGATTCTAATAACCTCAATTTCGTGAAAAAC[T/G JAACATGCCCTCAAAAAAGAGGGGAAAAACITTAACAGAAACACCTGCTGACATGATTAGCTT
EST37452 4	46 G A ---			AAGACATAAATCTGCAATGAATCAGTTATGAAATATTAAACCTCT[G/A]CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAATCAATGACGTAGAA
EST37613 6	34 A G ---			CTAGGCATGGGGCTTTACAGTCATTTATTACCG[A/G]GTCATGAATTCATTAATAAACACACGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCCAAATCACCCCTGCGTTCATGGATCTTCCATTCTAA
EST38025 4	56 T G ---			TTATTGAGTAGTACACTGTGGCCAGAACTAAGCTTTACATGTTTATATCACTTAT[G]TTATCTCA ACAATCTTGAAAGGGTGGTATTATTTCCCGCTTATAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57 C T ---			TCTACCAGGTCACCAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACCTA[C/T]CGCATGG AAGAACGCTCTCTTTTAAATCCCTAACTCTCTTCTCTGGAAGACAGAACGTCACAA
EST38420 6a	100 T C ---			TAAATCAAGGCCCTCTTTCATTACCAAAACAAAAACAAAAAGGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTACCTCTGACTGAC[T/G]CTCCCTGCAGTGCCCATGGGTCCTCCGTGCCT TATTCATTCTCTCTCTCTCA
EST38950 5	25 T C ---			TTTATTTGCAAAAGTAAGCAGCCGGT[C/T]GGTCCCTGGATTGAGGTGAGGAAGACATTACTTCTCTG CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGAGGAACAAAAAGCTT ACAACAAGAGCAGCCA
EST39053 6	90 T C ---			TTTTTGTACTCTGTAGCCAGTCATTAATCTGAAGTTTAAATATATCATTTTATTGGGATGAGATCA TAGTCTTTACACAAATGCTATG[T/C]AAACAAGTTACTGAATAATTTTACCTCGTGGAGTTG
EST39331 1	70 G C ---			TCCTTCTGCTCTAGCACCTCAGACCACCAAGAAAGCCTGGAAGACCAAGCATGGAAGGAAAGTA TG[C/G]GTGTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31 C A ---			GTCACCATTGACCTTACATAGTCCCTCTAGT[C/A]ACCTATGAGGCACTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAATTT
EST40548 4	37 T C ---			TTCTAATAGCATGCCCTGTGACAGGGAACTAAGCTCT[C/T]CAAAAATAACTGAAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCTTTTGTAGTTTCTCCAGAAGGCTCAAGGTGTTCT AATAATCTGTGGGACTCA
EST40549 1	42 A G ---			TGTTTCTCTAGAGAACCCCTGTGTGATACACTACGCGATGCACA[A/G]ATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTGTTACCACCATTTCTCACTTTGAACCTAGCTCCCTGCAAAAGCACCTTCTA CCCTGCACCTTTTGGGGAG
EST40579 1	81 A C ---			TGTGAATTACACATCAGTAAGGCAGTTTACAGAAATTTTCTTCTTACCTAAAGTGTGCTATCTCTG AGCTGGTGGAAA[A/C]GGACTTTGGAGACAGCGATTAAATACGGAACAAGGCTCTCCAGGAAG
EST40584 3	68 A G ---			TTGTATGGTTGTAGGAATTTGGGAAGAAATATCTGTGAAGGAAATTTGCCACTGTAATGCACACCC A[A/G]TCTGTACTCTCCACAATATCCTATGTTTAAAGCT

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EST51340	51 G A ---	---	---	GATCAAACTGTATTGCCCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 T C ---	---	---	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCTTTATCCAACTCTCGA[ T/C]TTTCCCTTGGTCTCCAGTGAAGGGAAAGCCCATGATCTTCAAGCAGGGAAGCCCCCAGTGAGT AGCTG
K01506	63 T C ---	---	---	CTGAACCTCAGCTGCCCTACAACTCCATCTCAGCTTTCTTCTCAGTTTCATGTGAAAACACTAC[T/C]C CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGCTCTATCCATTACCTCAAGCAGTCAATTCCT TAGTAAAGTTTCCAACTAGAAATTAATGACACCTTTGGTAGCACAATAATATGGAGATTATCCTTTTC ATTGAGCCTTTTATCCT
L18877	69 T C ---	---	---	TGAGTCTGAGCACGAGTTGCAGCCAGGCCAGTGGAGGGAGTCTGGGCCAGTGCACCTTCCAAAGGCC C[T/C]ATCCATTAGTTTCCACTGCCCTCGTGTGACATGAGGCCCATTTCTCACTCTTTGAAGAGAGCAG TCAGTATTGTTAGTAGTGAGTTTCTGTTCTATTGGATGACTTTGAGATTATCTTTGTTTCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---	---	---	GGTCCAGAACCTCTCAGCCAGGAGGAGCTGCCCTGGAAGGGACCTGAGCTGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAGACTTGACTGGGCAACACCCAGCGTC.CCCAC CC[G/C]CGTCGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTGACCCCTCT CTCCTAGAGACCTTGAG
L38517	137 G C ---	---	---	ACTTGAGAAGCAGAGCTCGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAATACAGTAGTCTTTTGTATTTTGTATTT[G]CGCCTGA AGATCATCCCGCAAGGCAGGCTGGAGGTGCCGGTGGGCTGTGTTGCTGGGATTTTGTCTGTGCTGG GAG
L39059	123 T G ---	---	---	CAAAGTTGTCTCCTGCCATGAGCACACACAGTCAGGCCCTTGAAGGGATCTCTAGGGAGACAACAGC CCTGTCTCAAACTGGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGCGGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCACACCACAAATCTGAAC[G/A]TGCCTCTCCCTTGTCTACAAATGTCT AAGGT
L41268d	173 G A ---	---	---	

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L48728b	111	T C ---	---	AAGTGAACAGAAAGCAAGATGGATTGTTCTCTATAAAAGCACATAGTTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAGAGCTCAAGTTTTTGGTTTACTTTCAGAA[T/C]GAAGAAGCTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAAGCTCATCCTGTACCTTGGAGATCCA GTC
M18079	52	G A ---	---	GCGCACAGTCCAAAATACAAAATTGGACAGAAGATCTATATTGTACCAGAAGCT[G/A]TTTATTTCAACC CCATCAAGTATAAAGGTTACTGATTGATTGGTCTTTTATAAACAATTGGTATATTTCCATTCATGCCAA AGCAAAAGAAGTAAAAGCTAA
M19169	113	T C ---	---	TAGGATCTGTGCCAGGCCATTCCGACAGCCACCAACCCACTCCACCCCTGTAGTGTCCACCCCC TGGACTGGTGGCCCCACCTGCGGAGGCTCCCCATGIGCCTG[T/C]GCCAAGAGACAGACAGAG AAGGCTGCAGGAGTCTTTGTTGCTCAGCAGGGGGCTCGGCCCTCCCTCCTTCTCGCTTCTAATA GC
M21539	114	T G ---	---	TCACCTCGTTCACAGCTCCACCTGCATCTTCATCAAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCCTTAGCCTGTGATCTGCCCATGATGATCCCCGACAGCAAAA[T/G]GTTTCTTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAAGGAAGTCTCAGCTGTACCGGCCCTTTCAGAGCT TCTTTTGGGTGC
M26041c	173	A G ---	---	CCTAGCATTAATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCCTGACTTC CTGATTTTCTTTTCTCA[T/G]GTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157	A G ---	---	CCTAGCATTAATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCCTGACTTC CTGATTTTCTTTTCTCA[T/G]GTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45	C G ---	---	CCTAGCATTAATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCCTGACTTC TTCTGATTTTCTTTTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57	G C ---	---	TAAGGCAGCTGTCAAGGGAGGCCAGTCACAGTCCAGCAATTCACAACCCCTTGAC[G/C]AATGCT TGCCAAGCTGTTTTAAAGCCCAAGAACACCCCTTCTTTGTTTCCAAATTAACCTTTAGAAGAAACCCCA CAATAAAGCAATTCATC
M81695	34	G A ---	---	ACTTACTTAACCTCACCTGTCAAGGCTGACGGGA[G/A]GAACCACTGCACACCCAGAGAGGCTGGG ATGGGCTGCTTCTCCTGCTTTGGGAGAAAACGTC[TGCT]TGGGAGGGGCCCTTTGTCTTGTCAAGGTT CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTTCCTCCCAAAAGGACTTGACTTGCAATTTCTACC T

U06641d	166	CT	---			CTCCTCCTTATTTCAGCATGGAGGGTTAAATGGAGGATCTCCTTTCTGTGACAAAACATCTTTC ACAACTTACCTTGTAAAGACAAATTTAAAAAGATCTTTTCACAACTTACCTTGTAAAGACAAAAT TATTTCCAGGCTATTAATACGTACTTTAG[C/T]TGGAAATATTCTATGTCAATGATTTTAAGCTA TGAAATACAAATGGGGGA
U09607	39	TC	---			GAGGCCATTATGAGGGTCCCTACTTACAGGAACACCCCAAT[C/G]GACATTGCAATTTGGGGGGCTCCCG TGGCCTGTAGAAATAGCCTGTGGCCTTTGCAATTTGTAAGTTCAAGACAGATGGGCATATGTGCAG TGGGGCTCTCTGAGTCCCTGGCCCAAGAAAGCAAGGAACCAAAATTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82	TC	---			GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATCCAAAGGCCCTCATCTGGAGCCTC GGGAAAGTCTGTGCT[C/G]ACATCTGCCCGCCCTTCCAGCCCTTCCCCAGCCCCCTCTTGTCTTC ATTCAATCAACAAAATTTGGC
U10694	20	CG	---			GTGACATGAGGCCCATTTCTT[C/G]GCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCATCTCTGGTTCCTTGTCTATTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAAATGTTCTTTAATGGTCAGTTTAATGAACATTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162	TC	---			AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGCTATCTTTGTGACCTTGCACAAAGTTGTTAAC CTCTTTGTTGAGAAATTTCTCCATGGAGTAACAATATCTAGTTGGGAGGATAGTGAAGTTACATGT AAGCACAGAGGAAACAGCCAAAGAGAT[C/T]TACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTTACCTTCAGCA
U15555	187	TC	---			TTTCTGCCACTTTCACCTGGTTTAAATAGCCAGCCAGTCAATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTTGGAAAGAAATTAATAAGCAATGCTGAACATCAGGAAATGTAGATATCCGTACAGAGAGT TCCAGTAAAAATTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[C/T]GGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122	TC	---			TCCAATTATTGGTCCCCAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAAACGGAGATCCACT AAACGTCACCGGGATTAAACAGAACGTCCTTGACAGACTGAGCGATGACACCACACAT[C/T]TGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAGCTTTTCTTTTCTGGGAAACAACTGTCCTTGG AATTA
U18543	58	TC	---			GCACATGCAGAATAGACTCAGCCTATGTCTGATCCAGCTGGGTAGTTCTAGAACTTT[C/G]AGAAG CTCCATCTTTAATGTTTTTATTGTTATGTCCCTCCCGGCTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGATTAGCAATTAGGCACCTCC AAGGCTTTAGTAGAGAGAGCC

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U25975b	164	C A	---	---	TCAC TGCTGTGGCCTCATACTCTTTTCCATTTCTACAAGAAGCCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAATTGCAAAAAGAC/A/AAGATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAAGGAATTGTGGACTGA
U25975a	143	C G	---	---	TCAC TGCTGTGGCCTCATACTCTTTTCCATTTCTACAAGAAGCCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAACAC/A/GAAGAGAAAATTGCAAAAAGACAAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAAGGAATTGTGGACTGA
U25997	61	A G	---	---	CAGGAGAGGTTATTCACAACTCACCACCTAGTATCATTTTAGGGGTGTGACACACCA/A/GJTT TTGAGTGTACTGTGCCTGGTTTATTTTAAAGTAGTCCCTATTTCTATCCCCCTTAAAGAAAAATT GCATGAAACTAGGCTTCTGTAATCAATATCCCAACATCTGCAATGGCAGCATTCGCCACC. <sup>1</sup> 3CAAAA TCC
U28413	29	C T	---	---	ATTCTGACAGCTAAATTAGCCCTAAATG/C/TGGGTAATATTTTCCCTCATGTTTTAAATGAGGTT AATATTTGCATAAAATCTAAACAGACTTCTGTATAGTTATTTAGTCAAAATGTGTTCCCTTGATCC CAGATGTTGTGGCCTGGGAAAGCCCTCATTTGCTACAGTACAAGTAACACAAGTCGTTGTACCTCAGTT G
U30884c	89	A G	---	---	TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTGTATGATTTTGGGACCTGCCGTATAATCTGTT CTTCTATCCACGTTAGCCA/A/GJTTGTTCTTGATGAATCTATATGAGTCAATAGAACACAAATCTAT TGACGGGAAGTCATTAGAATGGCTTGATATCTGTGATGGCTTGAACTTGCCCAACAGTTGAACACAAAGT GCTGTCA
U30884a	34	A G	---	---	TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGC/A/GJTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATCCACGTTAGCCAAATGTTCTTGATGAATCTATATGAGTCAATAGAACACAAATCTAT TGACGGGAAGTCATTAGAATGGCTTGATATCTGTGATGGCTTGAACTTGCCCAACAGTTGAACACAAAGT GCTGTCA
U31216b	78	A G	---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCATGAGACGGCCTGCAACCAAACA GCCGTATCA/A/GJCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTTCAGATA CCAGCACCAAGACCCCTTTACAACGTAGAGGAGGAGGATGCCAAGCCGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70	G A	---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCATGAGACGGCCTGCAACCAAACA GCC/G/JTCATCAAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTTCAGATA CCAGCACCAAGACCCCTTTACAACGTAGAGGAGGAGGATGCCAAGCCGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT

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U31416c	76 GA ---	---	---	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G]A]CCACAAATCTGGTGCCCTCTCTCTGCTTACAAATGCTAGGTCGCCCACTGCGCTGCT GGAAGAAACACACACTCCTTTGCTTAGCCACAGTCTCCATTTCACTTGACCCCTGCCCACTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 CT ---	---	---	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C/]T]CCTCACGCCCAAAATCTGGTGCCCTCTCTCTGCTTACAAATGCTAGTGCCCACTGCGCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCACAGTCTCCATTTCACTTGACCCCTGCCCACTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 CT ---	---	---	ACGGGTACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCAACTCACATTTGCTCTCC AGACCGCAGG[C/]T]CCCCCAGCCTCAGGTTGCTGGAGCTGCACATGACTGCATCCTGCCTGCCAGG GCTGCAAGCAAGGCTTCTCTATCTGGGGAGCGCTGCTCGAGAGAGGCCGAGAGGCCGCGAGAAC ATGCCAGGTGTC
U37690	54 AG ---	---	---	GACCACGCTGAACCCACCCACCGCTGCTGCTGACCATGGGCCCTGAGCGTCTTGA/G]CCCCGAATTC ACGAGGCTGAGGCATCCGGAGCTGGCGTAATGCCTGGCCGCACTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTTT
V00540	39 TC ---	---	---	TGAACCCGTTTCAACATGGAAATGATCTGATTGACTAAIT/C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTATTCTCTATAACCCAGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAGGAAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 AT ---	---	---	TCAAGAAGGTGACTGCCCTTGATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCAATGIGGTTTTAAAT/V]A]CCATAAGGGAAGGTACCCACAC CAGTATCTGAGTCCAGTAGCTAAGACCCCTAGAATTTGGATTCACTCIGTTTTTCAIGTCTCTCT GTAACCCCTGAGATCATCAG
X52011b	148 CT ---	---	---	AGGAAGATCCCAACCGACCCCTCCTGGCCTAAITCCTTTAGATTAGGTCACATTACATTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTCAAAAGAAAAGTTGCGAAAATTCGG AAATCTGTTGTGCA[C/]T]GCTCAAAATGAAAACGCTTTTCGGCTTTTATTTTTTTTGGAACGTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118 AC ---	---	---	AGGAAGATCCCAACCGACCCCTCCTGGCCTAAITCCTTTAGATTAGGTCACATTACATTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTCAAAAGAAAATTCGAAAATTCG GCGAAATCTGTTGTGACGCTCAAAATGAAAACGCTTTTCGGCTTTTATTTTTTTTGGAACGTG CGAGTGGCTTAGGTCTAGCCT

X54741	24 A G ---	---	CAGGCCACCTGTCTTCTCTCCAC A/G TGACAGCTTCCTGAGTCACCCCTCTGTCCAGCCAGCTCCT GCACAAATGGAACCTCCAGGCCCTCCAGGACTGGGCTTGCCAGCTTGCCAAATAGCAAAGGCCAG GGCACAGCTGGAGACGATCTTGCTGGCAGGGCTGGCCTTGTCGCCAGCCACCTGGGCCCTTCTCC AGCAAGCAGTGC
X54869	99 A G ---	---	AAGCATTTGCGTTACAGTGCAATCAGATACATTTTATATTTCTTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATATGTTATTTGCTCT A/G ATACAAAATTTCTAAATCAATTTATTGAAATAG GATGCACACAATTAATAAGTACAGACATCCTAGCATTTGTGTCGGCTCATTTTGTCTCAACATGGTA GCCGTGCTGACACCTCCAGAACGCGAGGTGCTGGCGCCGTTCTGCCGGACCCGCGGAACCTCTC CTGCCGGAAGCGGACGGGATGGGCCCCAACTTGGCCCTGCCACTTGACTTCACCAATCCCT TCCTGGAGACTG A AACCTGGTCTCAGGAGCGAAGGACTGTGAACCTTGTGGCTGAAGAGCCAGA GAAATGTGAAGAATGTGACAAAGCCTTTAAGCGGTTGTCACACTTGATTGTATATAAGATAA T G T CATACTGGAGAAAACCTCCAGAAAGTGTGACAAATGTGACAAAACATTTTAATTAATCTCATACCTTA TTGCACAGGAAAGCAATTTATCTTGAGAAAAATTTGATAAAGAAATGGAAGAATCAATTAATATCTGCT CATATCTTAACATCAGCGAGTT
X66924	147 G A ---	---	CTCAACCCATAACCTCAACCACATCT C JATCCTCCACCCACATCCCACCACATCCACCTCCATCC CCAACCCATCTCATCCCCAACTACAGCCCCAAACCCAGCCCCAGACTAATCCACAGCCATCCCCAA CTCATCTCATCCCCAACTGCAGCCCCAAACCCAACCCAGGGCCATCCCCAAACCCATCCCCAAGCC AAACTCAACACCATCC
X80026	25 T C ---	---	ACCCAACTCAAGTCCAGGCCCGCCAGGCATCTTCTGCCCTGCCCTTGCTGGCCCCATCCAGTCCAGG CGCTGGAGCAAGTGTCTAGCTACTTCTCTG C JACCTTTGAAAGACCCCTCCCACCTCTGGCCTCA CATTTCTGTGTGATCCCCCACTTCTGGGCTCTGOCACCCACAGTGGGAAAGGCCACCCCTAGAAAG ACCCAACTCAAGTCCAGGCCCGCCAGGC A/G TCTTCTGCCCTGCCCTTGCCTGGCCCCATCCAGTCC AGGCGCTGGAGCAAGTGTCTAGCTACTTCTCTGCACTTTGAAAGACCCCTCCCACCTCTGGCCTCA CATTTCTGTGTGATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG
X80197b	99 G C ---	---	GGCACCCAGAGTGACCACAAAGTCCAGCAGGAGGCGGCCCTGCCGTGCCGTGTTCTTTT CAGCCCCGGAGAGGTCTGACCTGGGGCTTCTCAAGCCTCACTGCGCCACAGCTCCCGCCGCTCT CTTTCTCCCAAGC G AAACCAATGCGCCCTTTCACCTGCGCTGCCGTGCCAGGCGCGGGGCTT CTTTCAGAGC
X80197a	28 A G ---	---	ACCACGACCATGGTCTAAGGACATGGATCGGGTGCCCCAGACGTGTGCACAGGGGACCCCTCTGCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGCGCTT G GGGC ATCGCAGGAGGAGCCATCGGGTACTACGCAAGCAACACTCAAACTGTCCAGGCTGAGATAAATCCC GGGA
X85106	150 G A ---	---	
X87160	128 T G ---	---	

X87344	34 C T ---	---	CATCCCAAGGCAC TGGTGTGACTCTGCTTCCCTGTCG/ACTGACCCAGAGCCTCTGCCTGTGCACCTGC AAGCTGTGTCTACTCAGGCCCAAGGGGACTCTCTGTTTCCATCTCCCCCAGAGCCTGTCAAGAG AAGCATGACAAACAATAATCATTTACCGACTTTAGTGTCTTTT
X87838	179 G T ---	---	GGTGGCTGTATCTCAGAAAGTGCCTGACACACTAACCAAGCTGAGTTTCCCTATGGGAACAATTGA AGTAAACTTTTGTCTGCTCTTTTGTGCGAGGAGTAACAATAACAATGGAATTTGGGAGTGACTC AAGAAGTGAAGAATGCACAAGAATGGATCACAAGATGGAATTTA/G/TCAAAACCCCTAGCCTTGCTT GTTAAAAAT
Z14138	81 A G ---	---	GTTCGTGCCTCTACACAGGGGCCCTGTACAGTGAATGGTGCCATTTCGAAGGAGCAGCAGTGATGA CCTCCTGTGACCCG/AGTGAATGTGCTCCCAAGCGGCCCTGTGTGTTGACATGTGAAGCTATTTGAT ATGCACCAAGTCTCAAGGTTCTCATTTCTCAGGTGACGTGATTCTAAGGCAGGATTTGAGAGTTTCACA GAAGGAT
Z18859	191 A C ---	---	TAATCTCACCATTCTCAGGTATAAGTTCTATAAACAGGCTTGGGTAATCTGGGTAATTAACAAACAGA AAATTATAGTCAATATACCATGACATGAAGAAATGAATCCATTCTTTGGAGATGGAGTATACATGACT GCAACTGTATTTTCATACGTTCTTTTCAAAGTGGGATAGCTATTGCAGCTTAAAGAGC/A/C/CAGGTTTC CAGTACTGGTTTCCAA
Z23091	159 G A ---	---	AGAACCTGACCAGATGTGGCTCGGAGGGGAATCCAGACCCGCTGCTGTCTCTCCCTCCCTCCCTCC CACTCCTCCTCTCTCTCTCTCTCTCTCACTGCAACGCTTCCCTTCCCTCCTCCTCCTCCTCCTCCG CTCTGTGCTCTTCATTCTCACTCACTG/AGGGCCCGCAACCCCTCCTCTCTCTGTCCCGCCCTCTCTGGA CTGAGCTTGACGTTTG
11595b	125 A G ---	---	GTTGGCATTGTTAGTAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAAGTATTTTATCAAA GTGTGGTTTCTGCAAGGGCAGGTTTGAACCTGACCCCTAGTTGTGCTCCAGGACCTA/AGJGGGTGC TCACCTACCTTGCTTTGTGTGAAGGAGTGGTTTCCCATGACTGTTTAAAGTGACAAGTGCCATGG ATATCTACACCGTCACCAGACTAGATTGTCTCAATGTCCTTGGCTTGGAC
11595	125 A G ---	---	GTTGGCATTGTTAGTAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAAGTATTTTATCAAA GTGTGGTTTCTGCAAGGGCAGGTTTGAACCTGACCCCTAGTTGTGCTCCAGGACCTA/AGJGGGTGC TCACCTACCTTGCTTTGTGTGAAGGAGTGGTTTCCCATGACTGTTTAAAGTGACAAGTGCCATGG ATATCTACACCGTCACCAGACTAGATTGTCTCAATGTCCTTGGCTTGGAC
1241	131 G T ---	---	TATATCACATTAGTATGTCACCTGCCATGGTAAGGACTTTGATCAGTAGGAAATGAACACACTTTGAA TGGCTTGTCTCTTCAATAAAAGAGTGACATGATTGAACATGTGTTTGTAGATAAAGGGCAGCTTGT JGCAGGAGTGTTTAGGATGAAGAGAGAAGAGATTAAAGGAAGATCAGGAAGAAAAGTAGCAATGGGA ATGAAATAGGAGGCCCTGAGATCCACTGGATAATCTAAAAAACCAAGAGAAAAG



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1282	130 C T ---	---	---	GTGGATCACCACACAGTCTAATTTTCAGATGTTTTCAATACCCCTAAAAGAAAATCTTGATCCCATTA GCAATATTCCCTCATTCCCTCACCCTCACCCTCAGGCTCTCTTATCGCTATAGATTTGCCCTCTACT TGACATATCATACATGGAGCCATACATATGTGGCCCTTCATGATGGCTTCTTTCACCTGAGAAATA ATGTTTTCAAGGT
6810	68 C T ---	---	---	AGTATCACACATACCTAATATATTAGATATACACAATAATAAAATCACTCCCTACCTTGAAAACTTT A/C/TJAGAAAGCATTTTTAAATTTTACACACAAAGCTCAAAACGAACTACAAATAAGTCTAGTAGCTG TTACGTGCCAAGGGATAAGGCTGAACAATAAATTAACCCCTTTAAAAATGCTATGAACAAGTACAA TTTTCTTTTGAGTTCGCAGAGCAATGACCACCTAAGAAATATTTTTAAAGGC
6817	118 A C ---	---	---	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTCTAGTATTTGCTTTTGTATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACAATGAGCTGCAGGGTAA/CJTGTTGGATACCCCTG TGCTCTACTGGCTCCAAAGGCATTGAGGGATCATCAAGATGTGGACACCTTGTTGTTCAATC TTGGTTCAGGTGCGGCTGTGCAGATCGGCTTTTGGTTGGTTGCTTAG
6819b	212 C ---	---	---	CCATTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACCGCAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTAGCAAA CAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
6819a	166 G T ---	---	---	CCATTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACCGCAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTAGC AAACAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
681xx	39 A G ---	---	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[G]TTATACTATGGCACCATTTGGGACA CAGATTATATATGTCAGACACCCAGCAATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCTATGGT TTAACAAAAGAAATGAACGCTAGG
6972b	149 G T ---	---	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAGGAATGGTACCAGTTCCCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTGGTAACTATTGATTATTCG CACAAATTCAGA/GT/CCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCTCTGGTTAGTCTTGGGA GAGTGTATGTCTCGAGGAAT
6972a	122 A G ---	---	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAGGAATGGTACCAGTTCCCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTGGTAA/GJCTATTGATTA TTGCCACAAATTCAGAGCCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCTCTGGTTAGTCTTGGGA GAGTGTATGTCTCGAGGAAT

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7598k	210 A C ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATATTTTCCCGTATTTTCCT CAATGCAG[A/C]
7598j	208 A T ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATATTTTCCCGTATTTTCCT CAATGC[A/T]GA
7598i	192 G T ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598h	144 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[C/T]ATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATATTTTCCCGTATTTT CCTCAATGCAGA
759Jg	142 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATTATTTCTTG[A/G]GGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATATTTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATTATTTCTTG[A/G]GGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATATTTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATATTTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTAATATTTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAATCAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCA[A/G]AGGAAC TCAATGAAATAAGCCGCTAACCAAGATTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAATCAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAGGAAC TCAATGAAATAAGCCGCTAACCAAGATTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAATCAAAGTTCCTCTATAAATT[A/G]TGATTTACAAAAGACACCCAAAGCCAAGGAAC TCAATGAAATAAGCCGCTAACCAAGATTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTCTCTATTAGACATCTGCCAGCTCTCTGTA ATACITTAATGAATGGGTAGTCTATCTTCAAGGTCCCAAT[A/V]CCITGAGGTTCCCT
7598b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTCTCTATTAGACATCTGCCAGCTCTCTGTA ATACITTAATGAATGGGTAGTCT[A/V]CTTCTCAAGGTCCCAATTAACCTTGAGGTTCCCT
7598a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTCTCTATTAGACATCTGCCAGCTCTCTGTA ATACITTTATGAATGGGTAGTCTATCTTCTCAAGGTCCCAATAACCTTGAGGTTCCCT
8071	119 A G ---	---	AAATACAGAAATTTTATTAGAAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCAGGTGG AAAAATGGGTTCCCAATAAATGGAAATTTAGGGCAACAAGTCTAAAAGGCC[A/G]CAAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTGCATTTTGGCATTGTTAATCACTGAATC TGGGTTTCTCTGAAITCCACACAGAGCATGCACTACACAACATTTTATCAT
8467b	93 C T ---	---	AAGGCTTTCCTCTAAACATCAGTCCCTACGGAGAACTGGGAAATCCTGGATATTTGGCTTATCATT TGACGCAAAATCCACTTTGCTGTAA[C/T]GGTCACTCCGAACCTCCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAGTATTAGGAAAAATTACTG
8467a	70 A G ---	---	AAGGCTTTCCTCTAAACATCAGTCCCTACGGAGAACTGGGAAATCCTGGATATTTGGCTTATCATT TG[A/G]CGCAAAATCCACTTTGCTGTAACTGTAACGGTCACTCCGAACCTCCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAGTATTAGGAAAAATTACTG
8498	84 C T ---	---	AGGGTTCAAGGTTTGGTTTAAATCAGGCTGCACACCTTCAATCAATCTGACATCTCTATGTCA AACTGGCTTCAGCTAG[C/T]AATACCTTCAATTAAATCGAAAAAGAAAAATTTGCTTAAAGGAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGCTTTTAAATAAAAGGAGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCCTCAATACAGAACCCAGGAATGTAATTTTCTTAACCTCAG

WI-18562	29	G A ---	---	CTAAGGAAAAATTAATGATGGAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTCATTACATT TAGCATTAAATCAGAAACGA
WI-18618	51	A C ---	---	ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGCGGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTTTCGATGCAAAAGTATAATTGTAACCACAGTGCTCGCACAGTTC AC
WI-18683	22	C T ---	---	TAAGCTGTTCCAGGACTGGACT[C/T]GGTCCCTTTATTAGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAAATAAATTTCTCTCCAAAGCCTGCCCTGCAGT
WI-18520	75	G A ---	---	GACTTTGGTGAATTAATGCTTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTACCTACTGCCAACAAACACGGGCATCCACTCTGCTTCAA TGCCCTCTCCGTGAGAC
WI-18563	94	A G ---	---	AAATAAAGTTTATTGGCACACAGCCCAAGCCCACTGGATGACACATTTGCCACGGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69	T A ---	---	GTCTATTTCATTTAGCTAGACCCCAATTCATCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC [T/A]GTGCCATAATTTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCCGAG
WI-18723f	94	G A ---	---	AACTTATTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCAA[G/A]ATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71	T C ---	---	AACTTTATTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGGT[C/A]CAGGGTACATAGGTAAACCAAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96	A G ---	---	AACTTTATTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCAAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18619	44	G A ---	---	TTTATTACAATATTTAGGTGGCACAAATACTAACAAAGCTTCTGA[G/A]ACAGGAGGTAACATTCCTCA TAGACTTTGCCAATCAGCCAGAAAGTAAACTCGAAATA
WI-18715	76	G A ---	---	TTATTCAAAAAAGTGATATTGCAGAGGGTCTGGGGCTGTACATGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGGAAGGGTATTTTTTAATAAAAAAATAA TGGAGCTACAACACACCCCC
WI-18535	107	G A ---	---	GTAATAAAGTTTATTGGCACAGCCACGCTCGTTTCATTATATGCCATTGACATCTGCTGTGGCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCCAAAC CTTCTGTGGTCCCCCGTG
D17525	107	C T ---	---	AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCACTACTAGTTTTCAGTTCTGGCAGGTGAC TTCATCTCTTCGAACTTCAGTTCTTCATAGAGTGAAG[C/T]GCTATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAAAGATTAACTAATAGATGCATAGCACCTTAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAGGTGATGTGTCTACCGGACGACGAAG

DWU-133c	313	A G ---	---	TAATTGGCCACTGCCCTATTATTACAAAACAGAAATGCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACTGACAGAAATATTTGTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTGAGTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C ---	---	TAATTGGCCACTGCCCTATTATTACAAAACAGAAATGCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACTGACAGAAATATTTGTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTGAGTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T ---	---	TAATTGGCCACTGCCCTATTATTACAAAACAGAAATGCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACTGACAGAAATATTTGTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTGAGTTTTGAATTTAATAGTAACCTCC JTCCTAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T ---	---	ATGAGATCCTTTAAATCCTTCCATGAACGTTTGTGTGGTGGCACCTCCTACGTCAAACATGAAGTG TGTTTCCTTCAGTGCATCTGGGAAGATTTCACCTGACCAACAGTTCTTCAGCTTCCATTTCGGCC CCTCATTTATCCCTCAACCCCGCCAGGTTTATACAGCTCAGCTTTTGTCTTTTCTGAGGAG AAACAAATGAAGACCATAAAGGGAAGGATTTCATGTGGAATATAAAGAT
DWU-387	169	G T ---	---	GTGTATAAATGCAACTGTTGATTTCCTCAACATGGCTCACAATTTCTATCCCAATCTTTCTGAA GATGAAGAGTTTAGTTTTAAACTGCACCTGCCAACAAGTTCACTTCATATATAAAGCATTATTTTA CTCTTTGAGGTGAATATAATTTATTTACAATG/GTJAAAAGCTTTTAACTACTAAGTATTTTCA GGTCTTCAACCAAGTATCAAAAGTAATAACACAAATGAAGTGICATTATTCAA
DWU-447b	172	--- ---	---	ATTTAGTGTCTTTGGCTTAAAAAATCATTCGAAAAAGTATTCGAACTGTCAAGCTGCCAGTCAGAT GGGTGTTGCCATTTAAATCACTGTAAATTAATTAGTTTGATTAGAGCACAAGCTTAGCTAATCAA CCATTATTTTCAATTTGTTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGCTTTCTGTAG GCCTTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-447	85	A G ---	---	ATTTAGTGTCTTTGGCTTAAAAAATCATTCGAAAAAGTATTCGAACTGTCAAGCTGCCAGTCAGAT GGGTGTTGCCATTTAA/GJATCACTGTAAATTAATTAGTTTGATTAGAGCACAAGCTTAGCTAAT CAACCAATATTTTCAATTTGTTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGCTTTCTG TTAGCCCTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-476	63	C G ---	---	GTAATAATTCAGTTTTTTTCCAGTTCTCTTTTGTGCTGCTTCTCAATTAGCGTTTAAAGGTGAGC/GJAT AAATCAACTGTCCATCAGGTGAGGTGCTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67 A T ---	---	TCATACTAGGCGAGTATCTCTCTAGCTAGTGCCTACAGAAAAATCTATCACCATACAAAAATTA[ A/T]TGCAAGTATTTATGTTTAAAGCACAGGTGTACCGAAAACTGTGAAAACTGTAATTTATGGGTT CTATGATGCATTTTGCCTAACCTAGAGAAAAGATTGATAAATTTTACCAGCTTTGAAGATGGAT TAACTTTGACTTTGAGCTTTAAACTTTTAA
DWU-512	131 A G ---	---	AAAATCCAGGCAATTCGAATCTGTTTTCATGATTTATAGAGGGTTTACACAAAGTGCCACTTATTA AGAGCTTCCACAGTGAAGATGGAGAAGGTGAATGCTTTTGAATATCCAGATGTTGTTGGTC[A/G] TGCGTATGGAGTGAGCAGGTATGTTTGGCTTTGCTTGCACTGCACTGAAATTAATTTGCTATCAAGAGC AACTATGAACGGTTTTTATCAAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C ---	---	AACTGCATATAGATAAATTATCCAGGATGTGGCTCATCTTTTCAGCTTGTTTCTATACTGTTTGTA ATATACAGTTTTTGTAAACCATATGATTGA[A/C]AAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATTTCTTGCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAAAATCTAGTCTCTGATTTC
DWU-59	94 C T ---	---	CATTCTTTGTGAAGGTAATGGACTCACAGGGGAAGAACATGCTGAGAATGGAAAGTCTACCGG CCCTTTCTTTGTGAACGTACATTTGG[C/T]GAGCCGTGTTTCAGTTCCAGGTGGCAGACTCGTTTTG GTAGTTGTTTAACTTCCAAGGTGTTTACTTCTGATAGCCGGTGATTTTCCCTCTAGCAGACATG CCACACCGGTAAGAGCTCTGAGCTTTAGTGGTTAAGC
EST11	68 C ---	---	CTTGATCATGGGTGGAATTTTGTGATCTGGCTTCATGGGATGCATAAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T ---	---	CACACTGGCATCTAGGCTTCGCTGCATTGCAGAAGGAGAGCCAGTCCCTCTGGAGAA[C/T]G CTGCGTTCCCGAGCCCCACACCGGCTTTGCACCACACAGGCTGTTGAGCGAGGAGGTGGGTAAGACGT AGCTGTAGACCCCAAGCAACCCAGCCCTGGGACCCCTGGGGAGAGGAGCACITTTAGAACATGGAA AAGTGTGGTCATCCCATCATAGACAAGACACATCCTACATAATAAAAAGT
WI-18014	40 A G ---	---	TCCATTTACATTTGGTGGCATTTTGTGAATAGCTACAGAA[A/G]GAATGAAAGTGCACCATCAGAGT GTAATTAGGCTGTGTGACCCAGGAAGTGCTGTTAAACAGAGATTTCTCAAGGGCAAAAGTGGCTTCT A
WI-18036b	97 T A ---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAATACAAAAGAGAACATGATAAAATCTG ATCAGAGTGGAAAAATTTTAACTTCTTCATAA[T/A]CTGACAGGTCAAGTAAGTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTTAACTTCTAGAAATACAAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAACTTCTTCATAA[T/A]CTGACAGGTCAAGTAAGTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	TGTAAGGTGACTTCTATAAGCTTCCATAAAGTGTCAAACTTTCAATTTACTGAGATTATTTACGGCCAAT GTGT[C/T]TGTGGGCTGAGATTGATTATCAGCTGGGTAAAGTTAACCTGTTCTGTTTCA

WI-18063	105	G A ---				AGGCTTTAACTGATAACAAATTTGCCCTTTAATCACATACAAAACTCTGCACCTTTCATTCCTTCCTTC CCATGTTTCTGATTTGATGTAACCTTAAATTTGT[G/A]TCCCTTTAAACAATATACTGTAGCTGCA
WI-18078	86	A T ---				AGTTGAAAGATCAGAGAGGTTATGGTTGGTAGCTGAACCTCAGATTCAGAACTTGGTCCAGTGTG TTGTTTTTTCAGCATCAG[A/T]GTCCACTAGCCAAGTTGATCTCGCAGTATCTACATGTGGT
WI-18091	90	T C ---				CCAAAGCTCACTCAGTATTAAATCATCTGCTAATTTTCATCCTTTGTTAATCCATCAGACACTGTGGT TTTCATCTCTAGAAGTTTGACTT[C/G]GGGCTTTTTTATACCTTCCATATCTCAACTTGTTAAGC
WI-18119	38	T C ---				GCAATCTGTAACAGTTTGGTAGTGGTATTACAGAGGAT[C/J]TTGTAATGGATTGGAGTACTTTAC CACTATTTCATCTGCTCTGAATAGTTCACTAACCAACTACTGACAACAGTTTAATTTTGGTTCTT
WI-18142	66	T G ---				TTCAAGATAATTACAATTGGAAGGGGACCAATAATCCACTTTTTTAATCGAAAAAATATCTATATAC[ T/G]CCCAATAAACTCAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAAGAGGAAAA
WI-18178	68	T C ---				GCATAGGTTGAGGGGTGTACAAGAGGAGAACCAAGATTCAGTCCATGCCTGGAGGTTAGTCTGGGGG GT[C/J]CGGCGGGATGGACACACAGACAGACATAGATCTGGCATCTGATAGCAGGGGCATACAG
WI-18244	35	G T ---				TCAATCTGAAACTTGTCTAAGCCAGCATGGGT[G/J]GGGAGGTGATTATGGCTGGGGAAGATG GGCACTCACCCGACAGCAGCATCTAGCACACAGTGACAGGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G A ---				ACAGATGTCAGTTGTTGAAATGGGCCATTAAAGTATGGGGCTTTCTTGTAAAAAAGTCATTCCAAA AGGCTTGGCAAGAGTTTGTCTATACAACGGAGGACAGAGAAACATGA[G/A]CTGGGGAGTAGGCTCT GACAGAAGGTGGGCTGTC
WI 18261	26	G A ---				GATTGAAAGGGATTGCTTTATTAACT[G/A]TGAAGGCGTGATAGAGGAACTGTTTAAGATAAACAA CTTATAAATACCTCCCAATTGTAGAAGTGAAAGATTG
WI-18268	88	C T ---				TAGGAGGGAAGAGGAGGTGGCTGCCCTGGGCCCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAGC TTCCCTACTTCCCCCATAGAT[C/J]CCTGACAAATGTCGTCAGAAAGCCCTCCAACCTGGAAC
WI-18299f	107	C A ---				TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTGGTTGGCCAATTTTT ATCTATTTGGGTCTGAGAAATCCACAAATTTGA[G/A]TTCCTTTTGCCAATTTATGACATATTCTG CAG
WI-18299e	101	A G ---				TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTGGTTGGCCAATTTTT ATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATTTCTTTTGCCAATTTATGACATATTCTG CAG
WI-18299d	77	G A ---				TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTGGTTGGCCAATTTTT T/G]ATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATTTCTTTTGCCAATTTATGACATATTCTG CAG
WI-18299c	67	T G ---				TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTGGTTGGCCAATTTTT T/G]ATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATTTCTTTTGCCAATTTATGACATATTCTG CAG

WI-18299b	52 G A ---	---	TCACAAAGTCATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACTTG[A/J]TTGCCAAATTTT TTTATCTATTTGGGCTGAGAAATCCACAATTTTGAAGAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299a	48 C T ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAA[C/J]TTGGTTGCCAAATTTT TTTATCTATTTGGGCTGAGAAATCCACAATTTTGAAGAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18307	76 G A ---	---	TCAACTGTACCAAGTTTAGCAGCAAGAGGATACTTCCTTAGAGACTTTCAGTGGACTTAAACTCAG TTTCCGCTG[A/J]TGCTATGTAAAGCATCCACGATGGTTTATTGTAATCTGCAATCTGCTGGTCAC
WI-18324	72 C T ---	---	TTTGGTATGAAATCTTCTCTGACATTTACCAATCATCATCTTAACTCCGGGGGTGGGTACTGATT TATC[C/J]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48 T C ---	---	ATGAAAGTCACITTCATCAATAGGGTCAAGAGAGAAAGAAATGTTTCAGAT[C/J]TAAATCTATGAAAA GGTGTATCTGCTTGAATTTAAGAAACACACAAGTCA
WI-18395	77 G C ---	---	TCTTGACATGATCTGTGAATAACGTGATTGGTTGAATTTCCCTGGAAAAATTTGAAGAATAAATTG ATTATTCAAG[G/C]TGTGCATTTGGTTTATACATATCTCTCTCTCITTAATGCAAAAGCTATG
WI-18398	62 G T ---	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAAGAAACAACTCAAGGGTT[G/T] GATAACATTGCCAGTATAACCATTAATTCAAAACAGCAGAGAAATTTGGAGGATAATTTGTT
WI-18396	21 C A ---	---	CTCGTTGGTATCTCTCATCC[A/J]TTCCTTTTCGCTCTTTCTAAATTTAAAGAAAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACTTATCACTTATCAACTTGTACAAAGTC AATGAAAA
WI-18409a	20 C A ---	---	AAGTGGGAAAGAGGAAATC[A/J]TTTCTTACTAGAGATTTTTCCTTTTAACTCTTTTCAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAGCTCTGGGGCCAGAGGCCCCAAGTGCTA
WI-18442	62 C T ---	---	AAAAAGGAAAAAGAAAGGATGGAGTAAGAGAGAGAGACAGAGAGAAACAAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAAAGGAAACACAGAGAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18452	38 G A ---	---	TTGATGTTAATACTGTCTATTCTGGAGATCGGCTAAAT[G/A]AAAGCATAGTTATTATTAGCTTTGG TATATTCTGGACAGATTTAAACAAGTAAGACATATATCAACCTCATATTTTCCAAACCA
WI-18489	102 A C ---	---	ATATAAGCTGGAGACTGTGGAGGTGAGAGGCAGTGGGACTAGCTGTTGAAGAGAGAAATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAAACA[A/C]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
EST5b	93 A ---	---	CTGGTGGGAGGAAACAAATTTGGTATATTCATACAAATGGAAAACTTTCAGAAAAAAGAAAGGAA CAACCCACTGAATCACACAACATGGACAAATCTCAATCATTTATGCTGATGGGAAAGAAACCATTCAT TAAGAATACACAGTACAT



EST5	93 A ---	---	---	CTGGTGGGAGGAAACAAATTGTGGTATATTCATACAATGGAAAACTCTTCAGAAATAAGAAGGAA CAACCACTGAATCACACAACATGGACAAATCTCAAATCATATGCTGATGGAAAGAAACCAATTCATCA TAAGAAATACACAGTACAT
EST6	48 C ---	---	---	TTAGCTACTTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAAGCTTTTCTTCCCTTTTGAACAAGACAAAGCAAGCCACATTTTGCAATTAGACAGAT
EST8	158 A ---	---	---	GGACAGGAGCTCTATTCOCGCTGTGCAGCAGCGGCTGATGGACTGAGGCCCGCAGGGATAGTGGGCG CTCTTCTCAGGGGCTCTCAGGACCCAGAGCTGTTCCCTGCTTTGAGTTTCCCTAGAGCTGTGCGGCCA GATAGCTGTTCCCTGAGTTGCAAGCACGATGGAGATTTGGACACTGTTGCTTTGGTGGGT
WI-18740c	104 G T ---	---	---	TCCTCATTTGTTGGGATGATGAGAAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAAGT GAGAACAAATCTCATTTACCATCATGTATC[G/G]AGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI-18740b	96 C G ---	---	---	TCCTCATTTGTTGGGATGATGAGAAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAAGT GAGAACAAATCTCATTTACCATCATGTATC[G/G]AGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI-18985a	105 C T ---	---	---	CCAAAGTCTCCTGTTGCTCTAAAGAAAGTTTGGGATGGGAGAGAATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCCTTCAATTTACAGAGGTAGCACAC[G/G]TATCCAAACACAAACCCCTTCCCC TTTTAAATGATTTCTGTTCTAATGCCATAGATCAAGGCCCTCAGAAACCATTTGTGTTTCCCTCTT TGAAGCAATGACAAGCACTTACTTTACGGTGGTTTGTGTTTCTTAT
WI-18746	114 G A ---	---	---	GCCAGCAGCTGAAGTCTCTTTTCTCCTCTCGGCTGGAAGAACATCAAGATACCTTTGGTGGATCA AGCTTGTTGTAATTTGACCGTTTATATTACTTTTGTAATATTCTT[G/A]TCCACATCTACTTTCAGCT TTGGATGTGGTTACCG
WI-19112j	212 G A ---	---	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCTGGTTACGGCCAGGGGGAATATGCCAAGG GACCCCTTAATGGAAACACAGATCAGTAGTGCTATCTCATGACAAACCAAGAAACCGACGACAAA TCITTTGCGAGATTTCTTCTAGTGGCTTAGAACATGGCTTTTGAACACACGGTGATATCTTTGAG GGTGACAAGGC[G/A]TCTCTTCAACAGTTCATACCAACTGCTTTGCTCTAG
WI-19092	232 A C ---	---	---	TGGTGGCTGGCTAGCTAGTTTCTACAGAACATAATTTGCCTCTATAGAAGGCTATTCTTAGATCATGT CTCAATGGAAACACTCTCTTCTTAGCCTTACTTGAATCTTGCCCTATAATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGCTTTTGTATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCAATAATTTT[C/A]C]ATGATTAGCCGTGTAAC
WI-19057i	175 G A ---	---	---	CCCATTTATTATAGGCCAGTGTCTCAAAGAGTAGAGGAGCGTCTACTGGTCTTCAACTCCTTCA GTCTTCTGACGGCGGACTTTACCGTGACAGCGGAAGTGGTATTGTACGTCCAGGCACCGCAGCCACTG TCTTCATGAGGAACACACAGTGCAGATCCCCACAGCTC[G/A]TCTCTTCTATCTTGGTTTGGCCACA

WI-20103	168	C T	---			TGGGACTTCCAACTCAGAGGATGGGAATCCCAGCTCAAATGATACAGGATAAACTGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAAGTCTTATCCCAGATGGCTCCAGGTACAG TGGGCTTCTCTGGGCTGGAAGCTGGGTCTCCCA[C/T]TTCATCTCTGCTCAAAGCTTCTTTGAAGGAGC TGGTTTGACTTCAACTTGTAGAGCCTAGCCCTCATCTTTCAGTCAACTGGGA
WI-20441	111	G A	---			GCCTTACCCATTTTGCACATATATACATATGCACCACCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTTAAGGACAAGAAATGG[A/G]TTGAATAGTAGTACCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTTCACTACATCAGAGGCCAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGG
WI-19911b	116	A G	---			TGGTTACAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCCTTTTGAAGAACGT TTTAGTCTTTTAAACTGAGTTTAAAAAAAATAACAATGCAATTTT[A/G]ACACTGTTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165	A G	---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAA[A/G]AAAGGGAGTTTCCAGCGCCAGTGGTGAGC TGC
WI-20613b	156	A C	---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATA[A/C]AGTTGGAAAAAGGGAGTTTCCAGCGCCAGTGGTGAGC TGC
WI-19984	47	A G	---			CAGTAAAAGAGTGATTCAGATTGCAGTAATACACTGACAGGTAAATA[A/G]TATAACATTAGAAAA GCAAAATCTTTTAACTTAAGGACAGACTGAACCATCAGGTATGGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTTCCACACTGGAAAAATGAAGGCAGTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	T C	---			GCCAGTTGGAATATGCCCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTTCTTTGGAACCTCTGCACCGACTGTCCATGCTCTGTGGGGACTTACACATTCAGTTTGACAG T/C]TGAAAAACCAACTGGAGCTGCTTTTCCAAAGAAATGTTCTGTCTTCAATAGGAATCCCATG TTATTTCTTTCTTGCTTAAGCTCTTATATCTTTCAAAATGACCTAAGCTGA
WI-18846a	49	G A	---			GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCCT[G/A]AAGCTGGGAGCGT GGGCTCAGCAGGGCTGGTCACTCCCATCCCGTAAGACCTCTTCCCTTCTCAGCAGGCCCAACATG GCCAGACTCCTT
WI-18959	123	G A	---			AGCAGTGGCCTTATTCATCCCAACCAACCGCTCTTGACAGGCTGCCCTCTTGTGGCAGCAACGGC ACAGCTAATTTCTACTACAGTGTCTTTAAGTAAAAATGGTCGAGAAAGAGGCACCT[G/A]GGAAAGCCG TCCTGGCGCTTGGCAGTCCGTGGGACGGGATGTTCTGGCTGTTTGGATTTCTCAAAGGAGCGAGCAT GTCTGGGACACACAGACTATTTTAGATTTTCTTTTGCCCTTTTGCAACC

WI-20146	31	T C ---				TGAGTCTCTGTAAATTCATTGAGCAGTTAGCT[C]/C/CATTTGAGATAAAGTCAAAATGCCAAACACTAGCTCTGTATTAATCCCATCACTACTGTAAAGCCTCATTTGAATGTGTAATTCATCAATACAGGC
WI-18922	74	G A ---				TAGGAATTGGTTTACGCCCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTCACCCTGGACTTAAGC[G]/ATCTGGCTCTAATTCACAGTCTCTTTCTCCTCACTGATCCAGGTTCCCTCCACAGAGAGCCACCAGTTCTC
WI-18763b	53	A G ---				TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGGA/G/GTGACGATGATGTGA/G/GTATTTAGAATGTACCATATTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18763a	38	A G ---				TGTTTTTGCCAA
WI-18771b	75	G A ---				TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGGA/G/GTGACGATGATGTGAATTTAGAATGTACCATATTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18771a	57	A G ---				TGTTTTTGCCAA
WI-18820	70	T C ---				CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCCTAGAAGATGTTGGGAACAGAAAGAAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18742b	51	C T ---				CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCCTAG/G/GAGATGTTGGGAAACAGAAAGAAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18882	94	C T ---				GGGAAAAATTTGAGACGCAATACCAATACTAGGATTTGGTCTGGTGTGATGAAAAATCTGAGGCC[C]/GTGATTTAAATCTTTTCAATGATGATTTCCCTTTAGGATATTTGCGCTAAGTGAAACTTGTCA
WI-19970b	167	G A ---				GTCA
WI-19970a	126	T C ---				ACAAAGTCCTGTAGCCCCCTCACCTTTCTGTTTCACTTTTGCCAATGT[C]/TATCGGGTTTGGTTTCTTGATTTAAACGGTTGTGGTTCCCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGAGTTTACC
						GTGTGTCCAAAAATGGGGTCTGCTCTGCTACCTTGACCCCTTCCCTTCTGCTCTCTCTCTCATCA
						TCAATCCCAACAACATCCTCTGCCA[C]/TACACAACAACAAACGTAAAGTTTCATTTGGGCAAAAAATTGAGC
						TATAAGCCCGAGTCAACGAGGAGCGCTGTCTGGCCACAGACAGGGGCTGCCCTGTGGAGCCTGCCCCACC
						GGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCCGTTCTGCGAGTTCCCTCACTGCGGGGACC
						AGCAAGGCCCTTCTCACTGGGTTGGTCAAAAG[G]/ATGTCACCTTGGCCCTGGTGATCCACAGAGGA
						TGTTGTTCAAACCCAGAAATCTTTAAACGACTGACCTTCCCTTAAAAACAGA
						TATAAGCCCGAGTCAACGAGGAGCGCTGTCTGGCCACAGACAGGGGCTGCCCTGTGGAGCCTGCCCCACC
						GGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCCGTTCTGCGAGTTCCCTCACTGCGGGGACC
						ACCAGCAAGGCCCTTCTCACTGGGTTGGTCAAAAGGAGTACCTTGGCCCTGGTGATCCACAGAGGAT
						GTGTTCAAACCCAGAAATCTTTAAACGACTGACCTTCCCTTAAAAACAGA

WI-19067d	202 T G ---	---		TATTGCTGCTTGCTCACTGCCTGACATTACAGGCGAGAGGCGAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCGAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAAAT/ GACATAGTATTCTTCTCTCAAGACGTGGGGGAAATATCTCATTTATC
WI-19067c	153 G C ---	---		TATTGCTGCTTGCTCACTGCCTGACATTACAGGCGAGAGGCGAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCGAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATATCTCATTTATC
WI-19067b	151 T C ---	---		TATTGCTGCTTGCTCACTGCCTGACATTACAGGCGAGAGGCGAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCGAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATATCTCATTTATC
WI-19067a	57 C G ---	---		TATTGCTGCTTGCTCACTGCCTGACATTACAGGCGAGAGGCGAGGCTGCTGCAGCCTCCGCTGGCTG TGCACATTCCTCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTT CTCTGGGCTCTAGGCTCGAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATATCTCATTTATC
WI-19106	247 T C ---	---		TTAATCCAGCCCTACCTTGTTAGTTATTTAGGAGACAGTCTCAAGCAGCTAAAAGTGGCTAATTC AATTTATGGGTATAGTGCCAAATAGCACATCTCCACCGTTAAAGACAGTGGATCATGAAAAGT GCTGTTTGTCTTTGAGAAAGAAATAATGTTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGGCCATAGCCTATAATTGGTTAGAACCTCCTATTTTAAAT/CJGG
WI-18944	147 A G ---	---		CAAGGCAAAAATATCAGGAGCTTTTACACACCTACTAAAAAGTTATTATGTAGCTGAAACAAA AATGCCAGAGGATAATATTGATTCCTCACATCTTAACTTAGTATTTTACCTAGCATTTCAAACCC AAATGGCTAGAAC/A/GJGTTTAAATTAATTCACAAATATAAGTCTACAGTTAATTATGTGCATA TTAAACAATGGCCTGGTTCAATTTCTTCTTCTTAAATAAATTTAAGTTTT
WI-18952	232 G A ---	---		CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATGGATGTTTCATAATACATAAA GTTCTCTGTAATTACAATAATTAATGCCCCTCTCTCACAGTCAAAAGGAACTGGGTGGTTGGT TTTTGTTGCTTTTTTAGATTTATTGTCCTATGTGGGATGAGTTTTTAAATGCCACAGACATAATTTA AAATAATAAACCTTTGGGAAAAGGTGTAA/G/AJACAGTAGCCCCCATCACAT
WI-18932d	177 C/T ---	---		CACACCTCATGCTAGCCTCAGAAACTGGAATAAGCCTTCGAAAGAAATGTCCTTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAAGCTTGTGCTGATTTGACCTTGATTCAGTTAACTGTCCCC CTTGGTATTGTTTAAATACCCCTGTACATACTTTGAGTTCAA/CJGCTTTAGTACGTGGCTTGGTCA CTTCGTGGCTGAGGTAAGAACGTCCTGTGTGGAAGACAAGCTGTGGCTTG

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WI-19042	193 A C ---	---	---	TTTGTACAGTGTGCCTCGCAATGCCCTCAGTAGCATCTCAGTGGTGGTGAAGTTGGAGATAGATG GATAAGGGAATAATAGCCACAGAGGTGAACITTTGTGCTTCAAGGACATTTGGTGAAGTCCACACAG ACACAATTTATCTGACAGAACTTCAGCATTTGTAATTTATGTAATAACTCTAACCA[A/C]GGCTG TGTTAGATTGTAATACTATCTCTTTGGACTTCTGAAGAGACCACCTCAAT
WI-18984	208 A C ---	---	---	ATTGGCCCTGTACAGTTTGCTTATTTATAAATTCATTAATAACACTACAGGTGTGAATGGTTAAAA TGAGGCCCTCCAGTTTATTTTCAGTTATTTTCAGTGTGCAGACAGCTATTTTCGCACTGTATTAAT GTAACATTTAATGAAATCAGAAAGCAGTAGACAGATGTTGGTCAATACAAATATTGTGATGCATT TATCTT[A/C]ATAAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGACT
WI-18851	90 T A ---	---	---	GCITCAATTGGCGATTGATTCAGTGCCCAATGTAACAGGGTTGGTAGTTGTACTCATTTTGAAT ATACCTTTTCCATTATGTATTCTT[A/G]TAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---	---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[C/G]GGGGTAGCCATTGTGCAGTCATGCCCGGGGGAACCTTGCCAACCTTCGTGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---	---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A[C/T]AGAGGCTGGGGTAGCCATTGTGCAGTCATGCCCGGGGGAACCTTGCCAACCTTCGTGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---	---	---	ACTCCTCTGCTGCTGCCAT[C/G]ACTGCTCTTTGAACCAGGAAAAGTCACAGAGTTTAAAGAGAA GCAAAATTAACATCCTGAATCGGGAACAAAGGGTTTATCTAATAAAGTGTCTTCCATCACGTTG CTACCTTACCCACACTTCCCTCTGATTTGCGTGAGGACGTGGCATCTCTACTTACGTACGTGGCATAAC ACATCGTGTGAGCCCATGTATGCTGGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70 G C ---	---	---	TGGAATTTCCCTTCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG[C/T]TAGGGAAAACATTCCATCCTTGAGTCAAAAATCTCAATTTCTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---	---	---	CACGGTTCTCTGCATCGTTACAGAGCGCCTTCTGGTCTAGCCAGCCCTGTATGACCGGCAATA TCCCCAAAGCTTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGTCATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGAGGTGG
WI-19037a	47 C A ---	---	---	CACGGTTCTCTGCATCGTTACAGAGCGCCTTCTGGTCTAGCCACG[C/A]CCTGTATGACC[G/C]GCAA ATATCCCCAAGCTTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGTCATTTCTGGAGAGGG GTCCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGAGGTGG
WI-19064	66 T C ---	---	---	TTGAGGAGGTGGGGTGAACCTGCTCTTGGCAGGGATTGTGACACTGCATTGCTGGGCTGTGTTCC[T/ C]GGGCTCTTCTGGACCTTGACCGTGGATACCAGGCCATGTGCCATGTTGGTCTCTGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---	---	AGGCCTGTGGCTTATGTACCCCAACAGAGGGGCTCTGAGAAGTCTGGCTGCCTGGGATGCCCCCTGC CCCTCCGGAAGGCTCTGCAGAGATGACTGGGCTGGGGAAGCAG/GJTGCTTGCTGGCCATGGAGCC TCATTGCAAGTTGTTCTGAACACCTGAGGCTTCTGTGGCCACCAGGCACCTACGGCTTCTCTCC AGATGTGCTTTGCCTGAGCACAGACAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184 C A ---	---	GTTTGAACCAACATGTGCTCTTTTTCAGTCATTCACTGTTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTTAAACGAAGTTCAAAGATTAGAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGACGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTTGGGGCTGGATAGTTCTCTGTGTGGGGGTTTGTCTTGTCACCTGTAG
WI-19016a	161 C T ---	---	GTTTGAACCAACATGTGCTCTTTTTCAGTCATTCACTGTTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTTAAACGAAGTTCAAAGATTAGAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGAC/GJTGATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTTGGGGCTGGATAGTTCTCTGTGTGGGGGTTTGTCTTGTCACCTGTAG
WI-20096	21 T C ---	---	GGTTTGGGGGCAATTTATTC/CJGATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGCCCC ACCCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	TGGGGCAATTTTAAACAAACCCAGGCAAAATATACATATACCTGAATATAAGGTAACCTCAAGCATG AGTATAAGATTAAAGGCAGTTACTTTTAAACAAAGGAAGTGGCATAAGCAACTCAGTGTGCCC CTTAGGTGGGAGCTCTTCCC/CJACTACCACCTCCCCACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---	---	TGGGGCAATTTTAAACAAACCCAGGCAAAATATACATATACCTGAATATAAGGTAACCTCAAGC CATGAGTATAAGATTAAAGCAGTTACTTTTAAACAAAGGAAGTGGCATAAGCAACTCAGTGTGT GCCCTTAGGTGGGAGCTCTCCCCCTACCCTACCCTCCCCCAAGGCATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---	---	TCCTCCAGCTCTGTCATCCTTGCTTGAGGGTCTGTGTTACGGCCCCCTCCAGGCATGGTTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAAGCCCACTCTCTAGAGGCTCCA/GJTCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATTTTATAGCGGGCTTCAGGAGCAGGTAGC AGGCCAAAGTGCACACTCAGGCCATCTTCTCTCCCAATGTCTCTCCCGGGG
WI-20860	224 G A ---	---	CTCTCCCTAAGGAGCCTTGGCCTTGCAGCCCCATTGAGGAGGATGGAAGTCAAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAAGCCCTTAGTATGCTGACATCTGCCCTTATCTCTCTCTCT CCCCAGTGTGTCACACTTGGGCAAGCAGAGTGGTGGCAGACCCAGCCTTGAGAGCTCTTGAGACC GGAAGGAAGGGCGGTCAT/GJAGGTGATGGCTCTGCTCTCTGGCTT
WI-19359a	39 T C ---	---	GACGTGGACAAAGGAGGTTTAAATGAATACTTTGTTTGT/CJCATGTTCAAAAAAGAGATTAAAT ATTTGTGACTGCATCTGTGAATGAAGACACTCAAAAAGCCATGTTTCCAACCTTAGGTTAATAATAA GGCTATTTGTCCACCCACTCTCGGGCATTTGCTGCAATATTCCTGGGCCCTCAAGTGGGAGGCCACGTG GGAACAAGGCCTCAGAAAAACAAAGGACATGCAGCCTCCCTGAGCCAGTTCTCT

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WI-19766b	93 A G ---	---	TGGCCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGG AGATGAACCATAGGAGCCAAAAGTC[A/G]GACAAACAGAAAGGACACACCAAGCCTGAAACCCCTC CGGACAAACAGCAGAGTTACCAAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTCAACCCCTCCTCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---	---	TGGCCTCAATGACTGGTACATTGGAGAAGCT[GA/G]GAGCAGCATCCTTTCTGTGGTGGCAGGGC AGGAGATGAACCATAGGAGCCAAAAGTCAGACAAACAGAAAGGACACCAAGCCTGAAACCCCTC CGGACAAACAGCAGAGTTACCAAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTCAACCCCTCCTCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---	---	CTTCTCTGTTTGGCTTGCATTGTGCGATTGTGGAATTTGGAAAAACCACTTGGAAAGGAGACTTCTCTGCAA AACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGAAGTGA[G/G]AAAGC TTAGAAAGGAAGTGAATTTGCTTCTTTGAATATGATTTAGGGCGGGCGTGGTGGGCTCACGCT TATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-20t:12c	59 T G ---	---	CTTCTCTGTTTGGCTTGCATTGTGCGATTGTGGAATTTGGAAAAACCACTTGGAAAGGAGACTT[GT/G]CTCTG CAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGAAGTGAAGCAAGC TTAGAAAGGAAGTGAATTTGCTTCTTTGAATATGATTTAGGGCGGGCGTGGTGGGCTCACGCT TATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---	---	GGGCTTAAATCCCTCTGTTGGGACTGGTCTCCAGTTTACAGCAAGGATCGCACCCCTTTTCC ATAACCCCTTCTACATTGGAAGAGCACACCTTGTATACAGAATGGCTCCGTGAAGTCTTTTAAACG GACAAAGGTAATACAGCTAACAAACGTCATGTTGGCTCACACGTAACCAACACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGGCA[C/G]TTCCAAAGAGTAACACTGCTA
WI-20679	82 T C ---	---	TGTTTGAATAAAAAATTCATGGTCTTAATTGAACGTATGTTACTTTCTTTTGAATATCCTTTT TTCAATTAATAATAT[CT/C]TAAACCACTCTATGTGTTCAACCTTCTGTTTAAACACTAAGATATGGGT TTTTGGAAAGGCCACAAAGTCACCAAGCTCCATGAAGTGGCGAATTGGTCTTGTTTTGGAAAGCTCTC CAGGGTGTCTCCAGAAA
WI-19909a	29 T C ---	---	CCAGAAATAAAGCCTGAATATTCCTTTCT[CT/C]TTAAAAATAAATTTTCTTTTCTTTGCTCTTCCAA GTAAATCTTAAATGAACCTGTTCTAGTCTATTTTAAATCTAGGCAATTATAACACTACCTAGGCGG TTTTTCTTTTATACCTTGTCTGTACGTGGGAATCAACTAA
WI-20341	221 G C ---	---	TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAGTGTCTTAGGGCATGAGACATTAGGAAG GCCACAAATATGAGTAATGAAATGTGGAGGCTGATGAGAAGCTACTGCTCCCATTTGTTTAGCAGGA GGCAGGAAAGTATCTGGGGTCTCTGGCAGCAAAAGCGTGTGTAATAATTTGGGTGACGTATGC ATCCCCCATGCATTGGTTT[GT/C]ATGCTCCAGTGAGCTGTGGGCAAGTCT

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WI-20113	60	T C ---			TTC TGG TAC ATG GTA AGT GCT CAG TAT TAC TGA TGA ATG AGC AAG ACG CCG TGA AAT ACT G[T/C] GGA AAC AGT AAA AAG CAA AAT ACC A C A C A A T T A G G A G G A A T T A T T T C A G A C A T A G G A T A T T A A A A C A T C A C T C A A A T A C T G G A G C A T G A T T C A G C A A T A A A T T C T A T T C C A T A A A C C A G G T A G A T A A A T G T C A C A G C T T T A A A T A T A G T T A A G T A C A G T T G A T C C T C G T T A T T C A T G G A T T C C G T A T T
WI-20895	107	G C ---			TGATGGCAAAGTACAAAGGCTCTGAAAGACAGAGTAAACAAGAGCAGCGCAGTGCGCGGTGTGGC CACTCCCACAGGAGCAACACTTGACTTCATTAAAGGCAAA[G/C]CTTACTCTGTTACTCTTTTTCCTC CCACATAGTTTAAACCCAAATAGAAAGGCAATTCATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATAACTGGTACTATAGGCAAAACAGATGCA
WI-20721	72	T C ---			CCTGCAATCACAAAAGTGAAGTGTGATATTTTGAATCATACTTTGATTTAACCACCTTCAGAAA TTC TAT[C] A A A A C A C T A G C A A C T T C C T T T A T C A G A
WI-19415c	161	A G ---			CTGGATTTTAATATTTCTGGCTTAATAACCAATGTATCAATAAATTTGGTCAATATCTCCACCTC ATTCTGCTAACATGTTTTCAGAGATTCCCTAAGTAAGGTATTGACGACTGAGACTAGTCCGGCAAA GTCATGAGACCCCTTAGCTGATCTCAT[G]AAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103	C T ---			GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCTG GCGGTGCGATGAAGAGACTGTTGGTCATGCGCGTGA[C]TGTCCCTTCTCCAGGCTCATATGGATGTCTT CGAGGTGCACAGGGAACCTGCTCTGCTTGTAGAAGCTTCTCC
WI-19348b	98	G A ---			GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCTG GCGGTGCGATGAAGAGACTGTTGGTCATGG[C]A/GTACGCTCTTCTCCAGGCTCATATGGATGTCTT CGAGGTGCACAGGGAACCTGCTCTGCTTGTAGAAGCTTCTCC
WI-19635	98	A T ---			ATTAGTTCGTGTGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAAACAATG TTAAAAGGTACAGTAAAAATACAGTATTAT[A]TATCTTATTGTGTAGCAGCGCTGTGAGGCTCATT GTTGAATGAAGCATCCTTAGGCAGCAGCAGTGAATGCATGCAGATATGTGTGCTGAAAAGAACTTTTGCCTT T
WI-19641a	46	A G ---			TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAG[A/G]TATTATAGTCTCATGTTT TTAATTTATGAATAACGCTGATTCATTTTGATTTTGTATTTACAGAAAGATGTCAGGGCTATCTCATTC AGTTATTAAATAAATGGATCAGAGTAGTAAGTCAAGAAATAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52	C A ---			ATATAGAGTACCATCCATGGTTTCAAGCATGGCTGGACACATTATCCCCCT[C]A/JGGGTAAACCAG GACTATTGCATGAGCATCTTTAATACGTATTTTGTATGGACACAAGTTTTCATGCTATTAT
WI-19673b	180	C T ---			TCTGCCATGATCACATTGTGATGAAGAACATGATGGTCACTAGTAGGTAACCTTCTGTGTCATTTGCCT TACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTTGGATCACCACCTGTAAATCTAATAGT GAAAAGGCAATGATGTCTCAGTATCACTGTGAAAACATTTTTC[C]TCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGCTCAAAAAAACACAGCCC



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WI-19673a	35 G A ---			TCTGCCATGATCACATTGTGATGAAGAACAATGATG[G/A]TCACTAGTAGGTAACCTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGCATCACCACCTGTAATCTCTAAT AGTGAAGGCAATGATGCTCAGTATCACTGTGAACAATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGAGCCTGAAGGCTCAAGGTCACACGTCACACGTCACACACACAGCCC
WI-19724	35 A G ---			TTTATTGGGAACAAAGGATTGTAATTTGGGTAA[A/G]CTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACAGAGTTTGGTTTCTCTT
WI-19307	196 T C ---			TCCTCTCCCCAACTAGATGGTATTGATCACTCTGCCCCACAATGGTACCCCCCTTCAGCAAGAAGCTG CAAGCCCTTCTGGATTGGCTTCATGAGAAATGGTGGCTTGGGATGGAGGTGACATTCCTTGTCTGT GGTGAACCTGCAAGAAAGGAAACCCAGGCAATGATTCATAGAGGCTTTAAAGAGACCCGTT/CJTG AAATGGGCCATGGTCTAATTTGGTGTGAAATAAACTAACCTCTTTGGCTG
WI-19289	85 A T ---			CTTCCCTCATCCCCCTTCCACCACACCATCCCGGAACAAGTGCTCCAGGATTCCTGCCACTGGC CATTTGGAGTGTCTC[A/T]TTGGGTAGCAATGTGGAACCAACCAAGGCTTTGTGGAGAAATGG AGGGGTTGAGGGAGTCCAGGAGGGCTTATTTGAGGGCTTTGCCACTTGTCTCATAGGCGAGCTCG ATCTCTCATCATCTGGACAGGTGGAAGCGAATCTTCCCGGGCTAGGCA
WI-19946	122 C T ---			CAATGGACTGAATGAGTGGTGGTGGGGTGGGGCACACACACCTTCAATACACGTCAGGTCG CTTCCAGTTTGAAGAACAGAAATCTGCATCTCAGCCTGAGACGCACAGAGAGT[C/T]TCTTCCCTG AOCAGACGCACTCAGAGCGAGTCTGGTTTCAAACTGCATTTAACTGCGCCAGAGAGTTCAC CGTAGGCATCTTTAATAACTAATCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141 G A ---			CACAGCATGGTGAATAGCATCAGATTGAATGAAAGTTTGTAAATGCAACCATAAATAATTATA ATAAATATACATCAAGTAACCTTACAGCACACATTTTATAGGGCCAAAGTTTGGATCTGTCTGGACCT CAATG[T/G/A]CTCTCGGAGAAGCAGCCACGTTAGCAGCAGATACCTTACAGCTTGTCTACTCTCAA GTGATGGCCCAACAGAGCTTCTGAACCTCCTCTGGGGAGGTAGCTGACAAG
WI-19076	40 G A ---			TTGGTTGGATACTTGTCTGGAAAAAAGCAGTTTAA[T/G/A]TATCAAAATACCTTTTAAAAA GTATCTAGCACAGATTTTCTGTAACTAGATTATGTTGAACTTTTCTAAATCTTGTAGGAG TGTGGTTGTTAAGAACTAGAGCTTATCCCTATCCAAATCTATCTTGGCTCCTGAAAACTGCAGA AAGGCATTGAAAGCTGTTCTTTAAGATATGGGATTTCTTTTATCTT
WI-20218	26 T C ---			CCACACACTCTGGTTTATAAAGCTA[T/C]JAGGACAGAGCAGAGATGGAAC TGAAAAACAGGGTAG AAAAAACAATAAATGGAGGGGAACAGTGGGATGCAGAAAGAAATGACAACAGCCACATGTGCCCA GTCAAATACTTTTAGTCCCTGCAGCAGAAAGATGCCAACCAAGTCTCTATACTGGCTGGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154 T G ---			CAACCTTTTGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAATATCTCCAGGCTTGATTGGGAGGGCTGGGCTACCCCTTCTTCTTCCCA TCCAGTCTATTGCCAGAT[G/C]CAGAGAAAGCGCGGGAAGCCAGCTCTCCAGCATAGCCACTGTGG GTGCGCTTACCTTCTGTGCACTCTCTGCTGGGACTTGTCTTTCGGGG

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WI-20361a	192 GA ---	---	CTGGGAGTGCTGACCTAAGTGACATTTTAAATGCCAAATACAGTAATCTCCAAAGCTTTTAATGGCTTATGCAAGATGACAGAAATATGTGAATCTGATTGTCCAGAGATTACACTCTGCACCTCCAAAGCTACAACAGTGCACAGCTGAGAGGTTCCCTATACCTCTACTACTGTGACAATTTAGC[G/A]ATCCTTCAAATGGGAAATTCCTAACTACACGAGACAATGGGTCTCTACAGTAGGCCCG
WI-20572	75 A G ---	---	GAGCCAAACCCAAACAAATAAAACAGAACTCTTTTGTAACTAAGTCATACCTACTCTTCTCTTCAGAAAT[G/G]TCATAAAACATCATCTTTACAACATGGAGAAGCGAGGTAGGCCATAATTTGTTCAAAATTCATCTTCTCAAAATTTAAATTTGTTTAAATCCCAAAGGTGCCTATTGAATTCCTCAAAAATAAATGCCTATCAGGTATCATACCTGCAATGCTTCTAATATCTCTTGATTAT
WI-20588	133 GA ---	---	CATGACAAAGACAAAGATCAAGGAGTAACATAAAATTAAGTTGAATAAATAGTATACAGCAATCTTACATTTTAAAGAAATGTGAGATCCTTTGTGGTTTTTATTTCCCTTAAGTACAAAATGCTAAAC[G/A]GGAGCCGAGCTCTCCGCATTCAGG
WI-20593	79 A G ---	---	TGACCTCATACTGGGTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTTGCTGACTTCAG[G/G]TTTAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAGAAAGCTGTTAAAGGAACTCAGGATGTTGTTAGGAAGGGGGAGTGATGCCAGGCCCTTCCACCAGACTATCCAGAAGCCATTCATGGGGTATTGGTCTGCATCTGTGAGACACTGAGCT
WI-19765	57 T C ---	---	TTCTTTGCCAAGCCTGTTCTCAAGTTATTCAGAACTGGGTGTATACCTTGCTCTCAT[G/C]ATGTATCTTGTCCTGCTGCTTTAGGTAGCAAGGTGTATGAATCTTTAAGTTTGTGTTCTTTCTCCTCGTGGTATCAGTGAATACTGATCTATTCTCTGGCTAGGGTCAATTTACAAAATTGCCATGGAACTGAGCAAAAGCCCACGTGGGATAAAATCACTCACCATCGACGCCACCAGTATT
WI-19066f	239 A G ---	---	TGACAAAGGGGAGAGAGGGAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGCGTTGGTGCACCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTACAGTACCATTCAGGCAAACTTTTCTTAAACGCCCTTCACT[G/G]GTTTCTTTTA
WI-19066g	184 C T ---	---	TGACAAAGGGGAGAGAGGGAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGCGTTGGTGCACCTGTAGCTGAATTAATCTCTCCATATTC[G/Γ]GGATGCTCAATTACAGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTA
WI-19066f	148 T C ---	---	TGACAAAGGGGAGAGAGGGAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAGCAC:TTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGCG[G/C]TGGTCACCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTACAGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTA

WI-19066e	147 G C ---	---	TGACAGGGAGAGAGGGAAATTTCTACTCATTGCAAGGAATCCTCACCTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAGCTGG CATATGTTCTTGCGJTTGGTCACCCCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAGTAGTTCTTTTAA
WI-19066c	100 G A ---	---	TGACAGGGAGAGAGGGAAATTTCTACTCATTGCAAGGAATCCTCACCTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAG TGGCATAATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAGTAGTTCTTTTAA
WI-19066b	87 C T ---	---	TGACAGGGAGAGAGGGAAATTTCTACTCATTGCAAGGAATCCTCACCTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAG TGGCATAATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAGTAGTTCTTTTAA
WI-19066a	72 C T ---	---	TGACAGGGAGAGAGGGAAATTTCTACTCATTGCAAGGAATCCTCACCTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAG TGGCATAATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAGTAGTTCTTTTAA
WI-20660	105 G C ---	---	TTTACAGCGAGTTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAGAAATGTTG TGCTAAATAAATCTCCCTTTTGAATGATATTTGTCGTTAATAAGGGAAGCAATTAATATTA CAGACATAATTACAAGGTTCTGAACATGAGTGATTCATTCTGTTCTGTACAAGATAGAACAAA AAGCTATCCACCCGCCCCCAAAAATACTGTTTAAACAACACTATGTTTAAAGA CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGGGGTCTCCTGGCAGCCTCCCTCAGTCTTCC TCCACCCGCCCTTCTCTCCAGCCTGCCCTGCATGCATGTGCACCCCTGGTC/TTTCGCTCCATCGCC TTGAAAGCTCTGAA
WI-19087	37 A G ---	---	TTCCCCAGGGTTCTGTATTGCAGCTAAGCTCAAATGTA/GJ/TATTTAACTTCTAGTTGCTCTTGCTTTG GTCCTTCCCAATGATGCTTACTACAGAAAGCAAAATCAGACACAATAGAGAAGCCTTTTCCATAAA GTGTAATTTAATGGCTGCAAAACCGGCAACCTGTAACCTGCCCCCTTTTAAATGGCATGACAAGGTGTGC AGTGGCCCCATCCAGCATGTGTGCTCTATCTTGCACTACCTGCTCC
WI-18790	49 A T ---	---	GAAAGCCAGAGATTAGCCCCGCAATCCGGATCTGTCAACCAGGACAGAAJATJGTCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACCTTGGAGATCAGAAAAATTCATATTTAAGCAAAGTGATACAAACA CAGTGATTTGGGAATGCT
WI-18987	35 G A ---	---	AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCTG/GA/JGTGGCCAAAGCCAGACACTCACCCACCTT CCCCAGTGGCCCCGTGGATCCTGGTCTAGGCTGGACACAGGATTCAGAAAGACACAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTGCACAGCCCCCTACACTCAAGGCTGAGAGGCCCTCAGGAA AGTCA

WI-18919	26 C T ---			TGGATGAAACACACAGGGATTCCGGA/C/TGCCAGACCCCATTTTATACCTTCTACAGTG TTGTTTGTTGTTGGTTTATTTTATACCTTTGGCCATACCACAGAGTAGATTGCCAGGTCT GGGCTGAATAAA
WI-18741c	64 G A ---			CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38 G C ---			CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23 T G ---			CTTCTGGTCAAGGCTTTGGACAT/GCTCTTCAGTCATCAGACAGAGTATCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170 G A ---			TCAGAACGACATGGCATCTGTTCTGCTTGGTTGGTTGGTGTACCTTTCAGGAGACCTGAATT TTAGAAITGCCAGTGTGCCAGAGTGAGTGAGTAAATTCCTTTTCAGGTAAAGATAGGCTATCTC AACACTGCTGAGTGATTCATAACATATCAACCA/G/A/TAGCATTAACCCATTTTATTTCTGTCCTT AGTCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	46 T A ---			CCAAAGTGCATCCATGTTTGAITTTCTGTGATGAGACTAGAGTGACAG/T/A/GTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATTATGCAGATGCCCTATGGAAATGACAGCTGC ATAATTAAACACATTATCAAGTCTCTTACAATTTATTTCCGCAGCATGTCAGCTAAGTAGACCCA ATGGGAGAGAAATGCCTGCTTCTTCCCTCTTCTGCACTGCCATAT
WI-19183	210 G C ---			CTGTTGAAGGCTTCTCAGGCCAACTCCAGCTTAAAGCCCTAGACAGTAAAGACACACATTGGATG GCAGCATGGTTTCTCCCATTTATGGCATGAATATGTGTTTGAATAGGAACAAGCATTAAT CCTTGCCAAACAGCCCTCACTTAAGAGGCTTTTGTGCTGAGTCAAGCAACACTTGCTGCTCTGCC CTTGGAG/GC/TGCAATTTGACCTGCTCTCACTGGTAAGGIGACTTGGTGGC
WI-20014b	214 T C ---			TTGAAATCCAGTCTCCTGGCCCCCAGGCAGGGTCTGTCCATAGATGTCTCTACTGGGGTC GTTCTGGCTTTTGTAGAACTTGGTCTGAGATGTTCTTCCCTGTCCATTCCATTGATGTTCTTT TGTTCAAGAGCAATGTTCTGTATTTCTGAACTGGAACTGAACCAAGTTTGCCTTTCTCCTAGTCACC AAGCATACTT/C/TCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198 T C ---			GTCTCCCCAGAGTGTCTTGACCCCCAGCCCTGTCTGCTGTAAAGGGGATACAGAGAAGCTCCCCG TCTCTGATCCCTTCCCAGGGGGTGGCTTAGTTGGACATGCTGGTAGCAGGACTCCAGGGCGTG CAGGTGAGCAGATGAGGCCCAAGCTCATCACACCGGGGCCATCCTTCTCAATACAGCC/T/C/G CCCTTGCAGTCCCTATTTCAAATAAAATAGTGTGCTTGCCTGTCTGT
WI-19135	20 G A ---			CAGTTACCTTGTCTTGCCTC/G/A/JAAGTGTCAATCAATTTTGTAAATTTAGTAACTCTGTAAAGT GTCTGTAGGTACGTTTATATATATAGGACAGACCAAAATCAACCTATCAAGGCTTCAAAACT TTGGGAAAGGGTGGGATTAGTACAAGCACATTTGGCTTACAGTAAATGAAGTATTTTATTAAC GCTTTGCCCATATAAATGCTGATATTTACTGGAAACCTAGCCAGCTTCAC

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WI-19236	54	G A ---	---	TACACAGAGGGTGGCACCTTGGACTCTGAGGGTGGGTGTGGAAGGGGGAAAGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTCCTGTAGCCGGTTTACATGGGAACAGGGTTAACATCTGTGTAGGGGAGGT CACCTTACCCCTTTTCATAGGGGAAGAGTGTACACTCCTGGCTATCTCAGGGGAATGGGAAAG AATCTTTCAAGGGCAAGAACCTGTTGGAGGATGCTGTGTATGTAATACT
WI-19144	222	G C ---	---	GTCCAGTCTTCCAGAAAGCAAGGACTGCCCTTCATTACAGCTTGTGACCTCCAGCCCTTCTAAGG CTCAGCCCCACGGGACTCTGTGGCTGCCAGCTTGTGAGCTATCTATCTATATTCATTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGGAGGCTGTAGCCAGGAACCCCTCTCTCCCTGGT CTGGCTGTGAGCGG[G/C]TGGGAACCAACACCTTCAGTGTGGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCCTGACAGAGAGTGGTGGCAGACACACACTAG[C/A]TTTTACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGCAGCATGTGGCGTCTCTGTGAAGCCACCGTGTCTCTTTGG GGGGCCGGAGATCTAGCATCTCTGAATCCTGGCTGTGGAGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA C/TJGGCAGATGCCCTGACAGAGAGTGGTGGCAGACACACACTAGCATTTTACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGCAGCATGTGGCGTCTCTGTGAAGCCACCGTGTCTCTTTGG GGGGCCGGAGATCTAGCATCTCTGAATCCTGGCTGTGGAGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTTAACATGAAGGAAAGGGTGCCT CATCCCAGCAACCTGTCCCTTGTGGGTGATGATCACTGTGCTTG[C/T]GGCTCATGGCAGAGCAAT CAGTGCCACCGTTTAGG
WI-19235	173	A G ---	---	TTCAGGAGGTGGAGTTGTCGTGAGCTCTCCTGCTGTGATGTGGAAGCTTCIGATATTTGAAGAAACA CGAATGTCTGTAGCTTCTCTTCACTGCCCCAGATTTGCTGTATTTATCAGCGATGCCCCCTGT CACTCATGCCCTTGCCTAATTGTTCACAATGGTGGAA[G/G]GCTTCATGTAATATGATCAGGACCCACC TCCAGTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCGACGCACTA
WI-19222	179	C T ---	---	CGTTTCCCTAACTCACCAGTTTAGTTTGGGATGATTTGATTTCTGTGTTGATGCCATTTCTAA CTTGGAAATTGTAGCCCTCTATGTTTCTGTAGGTGAGTGTGTGGTGTTCCTCCACCAGGAAGT GGCAGCATCCCTCCTTCTCCCTAAAGGGACTCTCGGGAAC[C/T]TTTCACACCTCTTTCTCAGGGAC GGGGCAGGTGTGTGTGTGTACACTGACGTGTCCAGAGCAGCACTT
WI-19117	134	A G ---	---	AAATAATGCAACGCAGGAGGAGAAAGAAATGCACCTAAGACAAGAACTTCTCATAGAACAATTG ATCTGTTTACAGGAACAACCTTGCTTGAATTTACACAGTGAGACTGTACATAATTGCATGAA A/GTJAGCTATTTTTCCTAAGACATTTTTCATTCATGAATATTTCAAGTTTTCATACTGTACA CATTCTTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAATTG

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WI-19134c	263 C T ---	---	CTCCTGTTCTGACCTGACAGGGTGACACAGCCCTTTTACACACTCTGTCTCCTATCTTCTCTGGGTAGA TGCCCTGGGTAGGGCTAGTACTGAATGGTCTTCCATCCCAAGAGGGGTGACGCCAGGGTCTAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACATATCCTTTTCAGAGCAC TTCATCCACTTGTCTCCTCCTACCTCGGCACCCCTGGTGGGAAAGGG
WI-19134a	162 T C ---	---	CTCCTGTTCTGACCTGACAGGGTGACACAGCCCTTTTACACACTCTGTCTCCTATCTTCTCTGGGTAGA TGCCCTGGGTAGGGCTAGTACTGAATGGTCTTCCATCCCAAGAGGGGTGACGCCAGGGTCTAG GCCCTTCAGAGCCAGGGCTAGAGGATTCACACGGTGGCTAGAGCCAGCTGCACATATCCTTTTCAGAG CACTTCATCCACTTGTCTCCTCCTACCTCGGCACCCCTGGTGGGAA
WI-19224	112 C T ---	---	GGTTTACCAGTCTTTCCAGGGAACTCCGATGAAGTGTCCAAACAATGAGCGAGTGAAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAAACAGAGGAGATAATCTTCACAGGATGCCTGTGAAGA AAGATCCCCTGGATCCAGGATGATTATAGGACAAGTTGTTCATAATCCAGCAGGCCAGAGACTTCC AGGGAAACTCATTCAGGAGGTGAAAATGATGGATGACTCTCCCAAGATGAAAA
WI-19201	179 T C ---	---	GCAGCTCCTAAGGACCACTGGCCATTAGCTCTTGTCTTGTATGGCATCTCTTCCACCTTGTCTCTC CTTTGCTCCTCTGTGTAGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCCTCACACTGCC CTTCCGCCCCCACACTTTGCCCTGCAGGTGCACCGAAAGGACTCCTGGGGGATAAAAATTCAAAAA GTGTGATGTCTGCTCAGAAAGTCCAGCTCCATGTCTGCTTGGCTTCA
WI-19034	45 T C ---	---	GAAATGGCTCCACTCAGAGCTACCCGGTGTATGAGGATAGGGAAATTCACCTTCTATTACATTAAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGCTGTTGAAAGTGCAATATAAATTTTGTG CTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTCAGCATTTAAGTTCTGTGCGAATTGAC ATTTGCTACTTATAAACTAGTCCCTAAGTCTTCTTATGCTGTCTATATA
WI-19102	25 C G ---	---	TGTTCTGAGTCACGCTGAGGAGAGTCGCTTCACTCAGGAGTTTCATGCTGAGATGATCATGAGTTCA TGCGACGTATATTTCCCTTTGGAAACAGAAATGAAGCAGAGGAAACTCTTAATACCTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAGAGTCTAGAACTCCTGTAAATTTTGAACCTCAAGGGAGAGGTAT AGTGGAAATGAGTGTGAGCATCGGGCTTTGCAAGTCCCATAGAACAGAAATGGG
WI-18548b	65 A G ---	---	AAAGGAGGGGAGAAATCTTTTACATAAATGCCTTGCAATCATCCTCCAGTCCCTCCTGAGGAA[A/ GJAAAAGCATCTNTCAAGCTTTTGCCCACTTTGGCTGC
WI-18548a	62 G A ---	---	AAAGGAGGGGAGAAATCTTTTACATAAATGCCTTGCAATCATCCTCCAGTCCCTCCTGAGGAA[G/A AAAAAAGCATCTNTCAAGCTTTTGCCCACTTTGGCTGC
WI-18700	97 T C ---	---	GGCAGCAGCTTTTAAATTTGAACACTTCTCTTGGAGGACACACCTTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTTCJAAAGATCCACAATTGCAAGGCCACTGCTGGCTCA CTTCTCACA
WI-18501	121 C T ---	---	CAGAGGGGAAAGTTTATTGATCAGCCACAGAGGAAACAGAGAAACAGACACAGAGGGTTCTGTGT GCATGGAGGAAATCAGGGCGCGNACAGCTGAACCTCGCGCAGGACAGAGGGCGCTGAGACAGCA GCGCATGCCACAACATTCA

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WI-18017	87	C A ---			ACAAAAGAAATGGAATAGGTTTGGAAAACTTATCTGCAATGACAAAAGTAATCCCGGTAGATAA GGAGAGGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCAATTAATAATATATCTCTTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101	A G ---			TTATTGCGTTCCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAAACGAAAGCA GTGATTTAGAAACNTCGATTCTGAATATCCC[A/G]TGGGGCATATGCAAAAGGAAGATGA
WI-18254	64	T C ---			TATACGGATCATGTATTGTGTGACCACCACCTACCACAGTCAATTTGTAGAGCAGTTAAATCAC[T/C] JGCCAAAATCCCTCTTCTTCTTGTAGTCAGTCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCGGTTCCTAGACATTT
WI-18265b	117	C A ---			CAATGGGTGGAGTGAATAAACCGCATATTGAGAACAAAGACGGCCTTCTGGCCNCTCTGCGTCC AAGCTGTAAAGGICTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG[C/A]GTTTTCAACCTTTC CTTGGGTGGTTCCTCAG
WI-18295	40	C T ---			ACCACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAAGTTGATTACT TCCTCTCCAAGGATGATGTTTAATGAATCCCTTNCCTTAGCTTCATTCTCATAATGCCAAA
WI-18459b	64	T C ---			GGGCAAGAGACAGAGATTTAATTGAATAAAACCTCCAGGCTGTGACACGGGTGGGAGACACAAAT/ C]GAGTAATTAAACAACATAATATTTANATGACAGTGCATTAATTAACGTCCTGGTAAAGCCAGAG GGGAGAGGAGGGCGTCTTCA
WI-22585	56	A G ---			TTTATTTAAATTTGCATCCTGAGATAATAAAATTTATCTGACAAGTGAACAAATG[A/G]CAGAAGC AGCAGTGAAAGTTTCGGAGAGGCGAGTATCCTTCATTTGGCACAGCTGTATATAGATTGA
WI-21155	36	A G ---			GGGCTGTGGAGTAACAGAACCTTGATGGAAAATTTGGC[A/G]TCTGTGTAGAAATGATTTCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88	G A ---			GCCTTTGCTCTTTGCTCTCAGAGGCCCTCAGATGGATACGCAGCAACTTCCCTTTGAACCTTTTAT TTTCCTGGCAGGAAGAAG[A/G]GGATCCAGGAGTGAGATCAGGAGGTTCTGTGTGACACAGACAG GGAAACAGGC
WI-19888a	98	C T ---			GGCAGGATTCACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTATTTTGATATGATG AAAAATTTTGGAACTAGAAAGTAGCAGTG[A/C]TTGGACAACGTTGTAAGATATTAATGCCACT GAACTGTTCATTTAAATGGTAATTTTCATGTTATGTGTATTTACACCTCAATTAAGAATGGAACATGT CTTATAATTGTAATACATGAGANCATATTTATGTGGAAGTGAACACAAG
WI-21485	82	C T ---			TGAGACCATCCTCCTCAACAAGAATCAGTCAGTTCAGCACCCTAATTTTCCACACACTGAAGTCTACG CAATTTTCATGCAG[A/C]TTGTGGACACAGTACAGTGCACAAATCCAGAGGGGCAACACATTTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125	T C ---			TCAGAAATGCTTTCCTGCTGCCCCAAACCAAAAGAAATTTAATGAATGNCNTTACAATGAGATGACTT GAAGTTAAAGAAAGGTACCTTCCTTGGAGGTTGCATGACAGGATAGTCTTCTGTGTT[C/T]CTTGGT GCAAGTTGAACCAAGTATGATGACCATTTGCATCAGAGCATCTGTTTCCCTGTCAGATCCCCACTAG

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WI-20561b	94	T C ---			CGTTGCTTATTTAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATG TACTTCAGATGAAAAATCCTTACATGTC[G]GGAATCAATGTCTTTTAAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAAATTGTAA
WI-20561a	25	A G ---			CGTTGCTTATTTAAGATGGCTGTTT[A]GJTAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTA TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAAATTGTAA
WI-20116e	69	T A ---			GCCTTCAATTTCTGTCAACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGCGGTTAGAACAT A/T[A]ATAAATCTATATCATATATTTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI-20116c	59	T A ---			GCCTTCAATTTCTGTCAACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGCGGTTAGAACAT CATATATAATCTATATCATATATTTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI-20116a	22	C G ---			GCCTTCAATTTCTGTCAACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGCGGTTAGAACAT CATATATAATCTATATCATATATTTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI-20466b	133	G A ---			AAAGATTTCAGTCTGGGACACAGTTTGGAAACACATATTTATAAGTTGCACATATTACAAACAG NTCCAAATGGTGAACCTGGTATTTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAACGGC G/AJTGGAACCTAATGTTTAAAAAGTTAGAGCTTGTCACAGTCAGTCTTAAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTTGGCTTTTATCCCTTICAGGTTTCGATT
WI-21444	39	A G ---			CTGGGCAGCAAGTAACCATTTTAAAGAAATACTCTCAAC[AG]AGTCTTTTATGGGGTATTTCA GTTGTTAAACAAAGTTAAATACTTATTGGAACATAATCTTTGTAATTTATTCGAGGAAGAAGATCT ATAAGATTGACTTACTCATTTGTTGACTGGTCTTTTGAAGCCTTACTGGGG
WI-21034b	148	T C ---			AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGTAGCAATTTTGTAGAAAGTGGTGATTAGAAGGATACAG CATAAATTTAATTGTAACATGCTTATCTAGCTAACCTAATCTGTTCTGTAGAATTACTGGTCTATGG GAGATTGGATAGATTCGCTTAACCTATCTCAATTTTAAAGTAATGTGAGCAA
WI-22091c	205	G A ---			GGCGTGTATTTGATGCAATGTCCAACCCAGTCAAGCTATCATTTGAAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCAATGTAAACATACAGCATATTACCTCCCCCTTAAGTGAAGTACTCATAATTC ATTACTTGTGCTGTAGCTTTTAAAGGTTTAAAAATGTAGCATTAAGTGGTATTTACTTTGAGGGCA ACA[G/A]AATACGGCTTAAACAACACACTAAATCATGAGGCTCAGGGATTG



WI-21805a	45 A T ---	---	CAACTGCTCTGAGGCTTTCACTAGCTGATTTATAATCCTATATTATJATJAAAAAATCTATAGTCTG CAGTCCTTTTGACATACCTCTCAAGGGTGGATATGTGGTGAATGCAGACTCCAGACTCCATCAATATGTGGTT TTGTTGCTTTTGAGCTTAACCTGCTTTAGNAAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATGGTTCATAAAAATCGAACAGTTGAAGGCTGTTTTGTAAATTGCTG
WI-21778b	155 T C ---	---	AAAAATCCATAATTATTGAACCCCAAGTTACAGAGAAAAGTTCGTAACCTTTTTTATTGAATTAATTGAC TCTGCCCGGTGCTGTGCTGCTTTCAACTCCAGTCTGTAATGCCCTGTGTAGGTGGGTGCCCCAG GTCGGGCTTCTGAGGTCCTGCGGTAGAGGAGGGCAGGTGGT
WI-20907	241 A C ---	---	TGAGTCAGTGTGATGGGGCAGTTGCGCTCAGCTCAGTGCCTGCTGACTCGGAAACACTGTGCCTCT CAATGATCTAGAGCTCATCTTGGGCGTACATGAGGGCAGTTGTTGTTCTAGTACCCATTTAGCCC ATGGCTCTCAAGCCAAATTCACACTGGGAAAACACACCCCTCACAAGATGCCTATCCATTTGAGTTT ATACAGGTTTTAGTAGCTAGAACTAAAAACATTTTTTA/CJAAATTATCTA
WI-21449b	222 C T ---	---	AACAGCAGCAGTCACCTTCCAAAAATGCAAAAAAAATTACAATTTTTAGAATAAAATTAATGTTTA TAATGCGGGTCAGAAGANTTGAAGGTACAACAGAAATCAATACAGCAGCAGTGGAGGCGGCTGGAG AAGCCAAAGCCCACTGCTCAGGGGTCCAAAGCTGACAAGAGTCCCAACCTGAGAGGTCTOCACAOCC AAATCATACCCCTCAGCTTCCCA/CJTJTGACAGAGCCAGTGTCTCTGGGTTAG
WI-21558a	157 G A ---	---	GCTTACAAGGAAGCCTGTGGACAGCGGAGNTGGGTGGAACCGACTCCAGCCTGGAAAACCTGCCCCTC CCATCCCCCTTAGCGCCTCTTGGCCTTCGGCTGATTTCTCGACAGCAGTTCTGGCCAGGGCAAGG AGCTGTGGTGGGGGCGAGTATG/AJAGCCAGGGACTCCCTTCCACAGATGAGGCCTAGGGCTGCAA AAGGGCCCCGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI-22187b	178 G A ---	---	TTTGCTGTGAATCCATGAGAGCCGGAAGCATGTTGGGCGGTGGCTAGCAGAGCTCATGNGACCA GTCTGGGCCCTGACCAATGGGTGATTACATTTAAACCAACCAACCAACAAACAAATACCAAGA ACAGATCACTGCCATGGACATCAGTAATCTATTGGTAATGGTG/G/AJAAATTTATGAAAATTTCC CCTAACCATAACAAAACTGTCTCTCTACCCCAAAAGTGTGGAGGAAAG
WI-22187a	110 C A ---	---	TTTGCTGTGAATCCATGAGAGCCGGAAGCATGTTGGGCGGTGGCTAGCAGAGCTCATGNGACCA GTCTGGGCCCTGACCAATGGGTGATTACATTTAAAAACCAAA/C/AJAAAAACAAACAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGGAAATTTTATGAAAATTTCC CCTAAACCATAACAAAACTGTCTCTCTACCCCAAAAGTGTGGAGGAAAG
WI-21609b	146 G A ---	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAAACGTGCAGTCCGTTCAACAGCTGTAAA AACAAAGCCCAACCCAGACATCACAGAGGCAAGCAGTGGCAGTGAGAGGGAGGCTGTAAAG GATGTTTCAAAG/GAJAGGGTCCCGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGCGAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

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WI-21609a	42 C T ---		TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAAAC[CT]GTGCAGTCCGTTTCAACAGCTGT AAAAACAAGCCCAACCAAGACATCACAAAGAGGCAAGAGCAGTGGCAGTGAGAGGGGAGCCTGTGA AAGGATGTTTCAAAGGAGGGTCCCGGCTATGTGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI-22512a	104 T G ---		ACATTCGGAGCCAGTTTTTCCATAATTGCTCCACTGGCTAAATCCCTTGGTGCCCTCCCTAGGGCTTCA GGGTAAAGCCCTGACATCATGGTCTTTGTGATCTGT/GIACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTAAGGGCAGGCAGCTACACTTGACTGCA
WI-21028b	139 A G ---		ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGGATATGTGACAGGGG TTTC[AG]TGCACTGGTACAGAACACACAGGGAGTTTCACAATTTTTTTATACAATGCTTGGGAAT CTACGG
WI-21028a	121 A C --		ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGG[AGC]TATGTGACAG GGTTTCATGCAGTGTACAGAACACACAGGGAGTTTCACAATTTTTTTATACAATGCTTGGGAATC TACGG
WI-18829d	58 A G ---		ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGNAATAACTTATGTGACTTCTTG[AG]TTTCA TCATACAAGACAAGCACAAAAGCACCCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-18829b	35 T A ---		ACAACATGCCTGTTACAGGGGGAAAAATCCTAGG[TA]AATAACTTATGTGACTTCTTGATTTC TCATACAAGACAAGCACAAAAGCACCCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---		AGCCAACTCAAGGCCAAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGAAGCAAGGA GCACAGGTAGTCCACAGAAAT[AG]AGACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAATACTAAGATTAGATGAACACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAAGGAAGC AGATGTTAACAAAAACAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI-20059a	59 T A ---		CTCTGAATAAGGGCCGTGAAGGCATGATTGGTTTGGCACACAGAGTGGATAACCA[TA]ACAT TGGCTGGAATGAGGTGAGGAGGAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGTAAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGCCCTTAGGT
WI-22130b	165 C T ---		TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGGGCTGCCCTTCCCTCTCCTGACAC CAGCAAGGGGGAGGCCACCATCACCAGCCCTGCCCATCATGCATCCATGATTACTAGCACTAGGAA GCCAACGGAANAGGACCCCGCGCTTGTCTG[CT]GTGTTTAACTCCAGGTTAAGCTATACAGGTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTGTGATGGGAATGAC

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WI-21661	117 GC ---				GCTTAGTCTCCACCCCTTTTAAATGTACTCTAGGTACAAAAATAAACATTATACACATATAAGATCAGTCTTTCCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAATA[G/C]TTTAGTCACAGTCACACAAAACACTACCTTCTAAGGAAAACGTCCAGTGAAGCCGTTAAATTTGTCCTTCAGCTATGAAGGA
WI-21980a	25 TC ---				TCAGTTTAAACACATTCATCAAGGA[T/C]AGATTAAATTAATGTCAGGTGAGCATAAAGGGAGATTAATAACCAGAAATGTGTTTTCTGGGAACCAAGTTTCAAGTCACTCAGGATAAGTTTTATTAAATTTTCATGGTGAAGCCCTGGGATAAAG
WI-21636	71 A G ---				TGCTTGATTAAATGTGGTGTACATTATCCTATTTTACAGATGGAACAGAAAAATACCAGCTTTTTTAAA[A/G]TAGCAATATCTATTATAATAATATTGAAATAACACCATAATAATATCACTAAGGAAGTAATCTAATTGTGTTGATTTGCAGAGGGAGAAACATTACCTCTAGAGCTGAGGCTATTGTGCTCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGACACAGGGATTTC
WI-22457a	112 GA ---				TTGCTATAATTTCTTAAATAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAAATCACTCATTAGACAAACAGTAAACATACTGGACACGGTTTTCAGGCATGAAGGATACA[G/A]CAGTTAATTAACTAAAGGAACAGAGTCCCTGCATTCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAAATACCTGGGGCCAAAACCCACTGAACCTACCCCACTGAAACACTGAAGGATACTGGGTAAAGGA
WI-21524b	97 CT ---				GCCGTGAGGGTTAGCGTATAATGAAAGGGTGAATAGCCGTGATGACGACCTTCGCGTCATCTTATAATGTTAATAACAGCATCTCTGTCTACCCGATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTCGCACTATGACAATGAGTTGTTGGAGTTGCGGTGTCCTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTTCCAGGGGATG
WI-21524a	35 A C ---				GCCGTGAGGGTTAGCGTATAATGAAAGGGTGAAT[A/C]GCCTGATGTACGACCTTCGCGTCATCTATAATGTTAATAACAGCATCTCTGTCTACCCGATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTCGCACTATGACAATGAGTTGTTGGAGTTGCGGTGTCCTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTTCCAGGGGATG
WI-22652a	32 GT ---				TTACCTTCCAAAACCCAGGCCACTTTGGAGAAAG[G/T]AAGAGAAATGCTATTAAATCAATAAGCCAAGACAATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACACCATCATCTCGCCACAGAACCTTTTGGACATGCTGCOOCTCCCTACTCCGCACTCAOCTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTTCTTTAGGG
WI-21703d	197 A G ---				CAACAGGCTCATGGAACAGAGCCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGGCTCTGCATCCCTTCTCTCAGCACAGCACCATCTTCAACCCTCTCTGGGAAAGCAGCATTTGGAGCCTACACCACTTGCTGCTTTTCTCACCAGGGTAAGAAATGCAGGTATTTCAGAGAGGGGAGTGAGTCTGGGAA[A/G]GTGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACTTGTGGGGGAAGAG

WI-21703c	134	A G ---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTCTGGGAGGGCTCTGGCATCCCTTTCTCAGCAGCAGCACCATTCTCACCCCTCTGGGAAAGCAGCATTTGGAGCCCTACACCAAG/C/TGTGCTTTTCTCACCAGGGTAAGAAATGCAGGTATTGCAGAGGGGAGTGAGTCTGGGAAAGTGGCAGAGCAGCAGCTAGGGCAAGGACTTAAGGGAACCTGTGGGGGAAGAG
WI-22663c	139	G A ---	---	CCCTTGTCAGTCTGTGCTCGCTTCTCACTGCACCTGGCAGGTGAGCCGGCTCGCTAATCTTATTC
WI-22663b	55	C T ---	---	CCAGTCTCGGTGAACATGGGTGAGTCTCTCCCGGCTCAGTGTGGGTTTGCACTGGTGCACTTACAGGC/G/A/GAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGAATCCCGTGTGAATGTGGGT
WI-22663a	38	C T ---	---	CCCTTGTCAGTCTGTGCTCGCTTCTCACTGCACCTGGCAGGTGAGCCGGCTCGCTAATCTTATTC
WI-22663a	38	C T ---	---	TTCCAGTCTCGGTGAACATGGGTGAGTCTCTCCCGGCTCAGTGTGGGTTTGCACTGGTGCACTTACAGGC/G/A/GAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGAATCCCGTGTGAATGTGGGT
WI-22668	99	A G ---	---	CCCTTGTCAGTCTGTGCTCGCTTCTCACTGCACCTGGCAGGTGAGCCGGCTCGCTAATCTTATTC
WI-22631a	52	T C ---	---	TTCCAGTCTCGGTGAACATGGGTGAGTCTCTCCCGGCTCAGTGTGGGTTTGCACTGGTGCACTTACAGGC/G/A/GAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGAATCCCGTGTGAATGTGGGT
WI-20258	157	G T ---	---	TCCTTTATCTGCTGCTGCCTGAGTATTCTGGGAATCCTACAAGGATTTGAGGGAGCCCTTGGGATT
WI-22714	212	C A ---	---	CCAACTTAACAAATTAGTTTCTGTAATATT/G/TCTAGTCCATTAGATTGTGTAATGATCTAAATGGNGTAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTTCGAAGAACTTTTATT
WI-22734a	44	G A ---	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTCAGTCTGAT/C/JAGCAACATTTTCAAGTTTAGGCAAGGTATTTAACCTCTCAGGGCTCATTTCTCTTTTGTAAATTTGTGAT/A/TGGACC
WI-22734a	44	G A ---	---	TATGTACCATCATAGGGTACTTGGACAAATCAACIGAAATTTT
WI-22734a	44	G A ---	---	AATCCACACTTTCACGGAGGGGACCAAGCTGCCATGTCTGCCAGGCTCACAGCAGCGGGGCTACTCTGCTGGTGGTTTGGTGGCAGGTGGAGATGGTGACGGGCGCATTTGAAACCGTAAGGCATGACAACG
WI-22734a	44	G A ---	---	GGAGGCCCGCGGGGTGTTTCAAG/G/TGCGGTGACGCAGGTGCATGGCTGGCAGCGGGGCTCTACAGAAGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTCCGGGGAAAGTACC
WI-22734a	44	G A ---	---	ACTACACATATGCTGATTTTCAACAGTAAAAATAACATTTTACATTTGTAGAGAAATCTAGGGTCT
WI-22734a	44	G A ---	---	ACTAAATAATCTAGTACTTTTCCACTCTCTGCTAACTCTGACAGGAGTGTGTGGGAAACGAAGTCTGAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTTT
WI-22734a	44	G A ---	---	ACCAACCCCA/C/A/TGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI-22734a	44	G A ---	---	TGGGGCTACTTTAGATGGGATGGCGTCAGGGTCTGGGAAGGCC/TG/A/TCTTAGAAGACATTACCCA
WI-22734a	44	G A ---	---	AATGATGAGAGGCAGCCAGTCGTGGAAGCCATAGTTTGGATGGCGAGACTTTTCCGGCAGAGGAAAT
WI-22734a	44	G A ---	---	AGCAAGTGCAAAAGGGCTGAGGGAGAAATGAACCTTGGGCTTGCTCCTACAGGGTGAAGGGCGCCGGT
WI-22734a	44	G A ---	---	NTGGCTGAGGTTTAGTGGATG

WI-22724	117 A G ---	---	---	TGATATGATGCTGAGATTGCTTCCAAATATGCTAGGAAGGGAAGAGTGTAGAGATATAGGA CAAAATCAAGATTGTCAAAATGTATAGTAACCTGTTAAAGCTTGCTAAAGGT[A/G]GTTATTCTATTTT TGGGATATGTTTGGGAATT
WI-22750	48 G A ---	---	---	TGTAACCTGTGTTTCTGAAAGTTGAGGGAAAGCTGAGGCAGCTAA[TG/A]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTTCTGACCATTTCTGACTGTGCT
WI-22775a	60 A G ---	---	---	TGCTGTTCTTTAGTTTATGACGTTTATCACAATGTGCTACTGTTCCTATTGTTTACATC[A/G]TAGTA GGAAAGGGAATAAATCCCTAAGGGCAGCAATAATTCTGCTTTTGAATCCTTCAATTCAGGCCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAACCTGAGGTATGTAGGTGTTGGGAGCCAGGAAAGGAAG GGT
WI-22808	143 C T ---	---	---	CTTTAGCTAATGAAACTGGCTATGIGGACTATGATAGACCAAGAAAGCTACCCAAAGTCCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTAGCAACACAGGA GGATGAAGA[C/T]AGCAAACTGATTAAGAGAGTAGGTATAAGAAACCCAGGGAGAGTGGGGTCCAAAT ATC
WI-21016	207 G A ---	---	---	TCTCTGCTGCTTGAGCCCTCATCCACACCCCTCCAAGCCCTCATGCCCACACACCGTGTCCACAAT CCCCATCTCCCTGCTGCTCCCATCTCAAGTCCAATTCOAAGGCCAGAGCCCTGGCAGCTTTTCTG GGAGACAGCATGAAAAGGAGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGCGCTGTGGGTG CTG[A/T]TGGCGTGGTGTGTTGGGGGCCAATCCTGAGGCCAGAGTTCA
WI-21031	31 C T ---	---	---	TGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCATTTGTCTCCAAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122 A T ---	---	---	CCATATCCAGTCTCTTTGAAGCTTTCTATTGACTTTTAGGGTTCAGTTATTATATATCCTTTTACTAT GACTTCATTGATTTTTTTATTTGTTTCTCCATTTCTCTGCAAACTTTTC[A/T]TTTGTATTATAA ACTGTTTCTAAACTTCATTAAATCTCTATCTGTATTTNCTTGTAGTTCCTGAACTTCTTTTAGAGG AGCGAGCATCAGAATCACCTAGAGGGTTGACTAAACACAGACTTCTGGACCCCAACCCAGAGCTTCT GATTCAGTAGGCCTGAGGTGGGCTTAC[G/A]AATTAGTATTTCGAAGACCTTCCTAAGTGTTCAG ATGCTGCTTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTTTCTTTTAAA GGAGAGACAGGAATTCAGAGAACTGCTAAATTTAAGCATAATGTATTGAAT
WI-21186	95 G A ---	---	---	CCACGATAACTATAAAAGCAGAAAATTAGCTTTGAAAATCAAAATAACATATTAGTAACACACATT CATTTTATAAACACACATAAAGACACC[A/G]GGNTCTCAGTAATGCTCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCAATTTCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGTGAGACCAAGCAACCTGT
WI-21187a	94 A G ---	---	---	

WI-21190	39 T C ---	---	TTTTCCACATACCAATGCACCTGTTGTATAAACTATTCGTCGGGTAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATTTATATTAACAAATAATTAATCTGTACTATTACTGC TTAGTTATCTAGTGTATTGAGAAAGGAGAAGTCAGCATAGTTATTTCCATGTAATAAAGCTT AACACA
WI-19937d	186 G A ---	---	ACCATGTGCATTTATGGCATAGGAATAGTGACCAAGAAATGCAGCANCTAAACTTGAAGGAAA GAACTATTGCACAACCAACATTTACATATCTGATTAGACAAGCAAAAGCAGCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATGGTGTGTTCCCTCAGCAAGTCGATCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCTTATGCCTCAGGAAGAA
WI-19937c	185 C T ---	---	ACCATGTGCATTTATGGCATAGGAATAGTGACCAAGAAATGCAGCANCTAAACTTGAAGGAAA GAACTATTGCACAACCAACATTTACATATCTGATTAGACAAGCAAAAGCAGCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATGGTGTGTTCCCTCAGCAAGTCGATCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCTTATGCCTCAGGAAGAA
WI-2117b	227 C T ---	---	GAAACGGGTGCTAAACAAAGAAAGTCTCAGATCCCACTGAAATCTGTTTCAGTTTCACAGGCTC TCTCCAGAAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAATACATCTGGGG TCCAATCACATCTCAGGTTTCAGACTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGATTTCTTCTACTGAACTTGGGTGGAG
WI-21122a	42 C T ---	---	TCACTTTGTATCAATAATCCCTGTAAAGCTAAAGTTATTCATC/TTTAACAGGAACCTGTTTTTCC TTATTCAAATGTCAAGCCTGACGCTTACTGTACATATTTGCTAGCAGGAGACAACCTGGAAATACT AAACAAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACACATAACTTCTT TTGTAGGTTTCACAGAGAGCCTATTTGTGGGTGCT
WI-21254	53 A G ---	---	CAGTTTGTGTACAGGAAGGGCCCATGAATGTGGGGGAACTATTCCACAGGAGAG/G]CAAGGAGAAG CTGTCTCTGG
WI-21054	23 G T ---	---	AAGGAACTGCATGGGTACAAATG/TTCCTCAATTCATACIAACAAGGTGGGAAACGGGTCAATCT TGGCTGCTCCAGAACAGGGCGAGTCTATGCACCTCTG
WI-21059b	181 T C ---	---	GGGACCAAGGTAAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGAAGAGACATACCTCACTGAAGTCATTTCTCTATTCT/C]ATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCTCTGCTTAAT
WI-21059a	63 C T ---	---	GGGACCAAGGTAAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGG/C]TT GAACTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGAAGAGACATACCTCACTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCTCTGCTTAAT

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WI-20442	37	T C	---			TCCACGTGAAGGAAGAAAAAANGGGGGGGGCTT/CJTAAGGTGGCACAATTTTAAGAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAACAAACAAAAGTCAAGTGATGAGACGAA CA
WI-21235	43	T C	---			GTGACAAGAGGTGAAGCAAGGACAAAGGGCAGCAGGGCAGTCT/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57	T C	---			ATCAGAACTGCAATCTGCACATGAAAGACCTGGGGGGAATGCCCTACATCTGGAATTT/CJCATTA ATCAACGTTAAATTTGTCCGACCAGTTCTTCATGCTGATCATTGATAATGACAGATCCCAACAT GAACTCCTGAAGCAATGAATATTTACCTTGTGCTTTCATGCAAAATTTAGGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACCAGATCTAAGGAATTTGACAGGGATCTTCT
WI-21149a	167	G A	---			AGGACCTGCTCTCACACGTTCCCTCACCCACCAGCTTTTGCAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTCTCTCTTTTAAACAATGACCTTATTTATCTTTAACTTTAACTGAGTCTTATATA CAGACCTGCCCAACTGGAAGCTTTTACACIG/ATGCTTCAGAATGCGGCGATTTGCACAATGGTT TGGGCGAGGTTCTGTGGTTAAACATGGGATGGAACCCAGGCTCTACCTG
WI-213, db	188	A G	---			GGTGCAACTTGGAAATAATGGTTTAAACACAGGATAAGCATTAAAGGAAAAACACTTTCAATGTGTC TTCCATTTGATGAATTTTCTCTCTTTATCCCGCAAGTGGAGTTTCATGCTCGGTGAAACCA GACAGTGAATCTGTTCCAGCCCAATCTGCAGCATTAGGGATGAGTTCTC/A/G]GAAGTGATTCT GAACTGAGCACGCATGCTGCTGATGGGGAACCTCTGGGGAGAAGAGCCT
WI-21382d	125	C G	---			CCATTGCAGTCCAGAGATGAGAACTGGACCAGAGGCAATCATGAACAGACGGGAGTCAAGAGA AGGGGTTTCTAAGATGGAGAAGTGGGGCGGGTTTGGATCCAGTGGGATNTGGTTCCTCC/CJGAGGTT GCAACCCCAAGGAAGTCTCTGGAAGC-A/GCACCAGTCTGATGGGGGAGCAGAGAGTGCCTCCTC AGTCAGGGTCCGAGTCCGAGGAGAGTCTGCTGCTCCATAGTCTCGCAC
WI-21437a	201	G A	---			TCCCTGAGGTTGGAGTCTAGCATAGTCTCCCTCAAGAGGGGACAGGGGTGAGGGCAGAGC AAAAATCCAGTCTGCTCAACCACGGAGACTGCCCTTTGGGATGGAAGTTTCTGGAGCTCCCTCCATT CTATTCCTGTGGGCGAGAACATGCCAGGGCTGCTGTTAAATGGCAGGGGTACCTTTTACCAGGGC/G /A/CAGGCATAGTGTGGCCCTGCTGCCCTGGGGGCCACCCCTGGGAACAGT
WI-21202b	156	A C	---			CAAAATAGAAATCTTTGTGAGTGGATTGACTTAAATTTTATTTCTGTATAAGCTAAATATGTT/CJGA GTTTTATGAACATGTATTTTATAAAAATGGTCACAATATATTTTAAAGTTAACTGATTTATGAGGG AGGAGGAGAGAGTTGACCAA/C]GTCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A
WI-21202a	61	T C	---			CAAAATAGAAATCTTTGTGAGTGGATTGACTTAAATTTTATTTCTGTATAAGCTAAATATGTT/CJGA TCTGTTTTATGAACATGTATTTTATAAAAATGGTCACAATATATTTTAAAGTTAACTGATTTATGGA GGGAGGAGGAGAGTTGACCAAAGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A

WI- 21627b	153 A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA/GJTCCAAAGTCATCTAATATTAAACCATATTTTACATAAATTTGTAGG GACAGTACTAATACTCTACAATAAATAAGGGTTTAAAAATGTGTGCTTA
WI- 21627a	106 A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTC/GJTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATTAAACCATATTTTACATAAATTTGTAGG GACAGTACTAATACTCTACAATAAATAAGGGTTTAAAAATGTGTGCTTA
WI- 21399a	75 C T ---	---	GGATTTGAGTCCCACTTGATCTCAAAATTCACCTCTTGCAATGTAACAAGCTCATTCCTCTAAAAGTT TCAGTTTC/JTTTACCAGTAAGGAAAGGTTGGACCAGACATGTTGGCCGTAATGCTTGGTAA CTGCCCTCTGCATTTGCTCTGAGGTGTGTGTCCTCCTAGGACTAGGTAGGATCTCTCTGCTTCTGCC TTACCTAGGCATAGTGCTGATAGCAGGCTGAAGCCCCAATTCATCTGT
WI- 20329a	68 G A ---	---	CGATGCTGCTAAGATAGGAGGTTAATCTTTACATGGTGGTGCACAGACAGACATCAAT C/GAJTCTGTTAGCAGCGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTGTGCTGCTCTTAAAAACAGTAAACCAATCAAAAGAAAGATTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGATACCACAGAGCCCTGGAAGGGAAGGCCCTCACT
WI-21249	155 T C ---	---	TTCTGGCATTCAAAATGTACATGTAAATCCAATTTAACAGATCAAAATGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAATCACAATTGTATCTAAGTTTCACTTTTAAGAAACATTATAAAGGTAATT AAAACCTAGGTGTACTATT/CJATGGAAC/TAGTTTATTTCCNATTTAACTACTGTTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTAAAGGAATTATAAACACATTGAGA
WI-21504	147 C T ---	---	TGACACAGCATCAATTTTCATGAATACCTTTGAAGGGCCATTAGAAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCACAAATTACAGTGGGGGACGGCGGTTCCGGCTCCAGCTGGGTTTCCC AGATGCAACAATTC/JGCGGTTCTGGCTTCTCCACTGGTGGGGATGGGGATCGCGCCCTTCGGGAGCTCT CAGGG
WI-21242	115 G A ---	---	CTGCACCAGGAGGACAGCTGCTGGCAGGGACTAATAAACCTTCCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAACCGCGGGCAGGGAGGGGCAGAGAAC[G/A]C/ACTAGCTTGGGGGTG GGCACCAGCTTCAGACCCCTT
WI- 21475c	181 A G ---	---	TAGCCCTTCTGCCAACATCTGGCAANTGAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTCACTTGTCTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGCAGTGGCTCTTTGGAGAAGGCA/GJAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTCCCGTTCTCCACCCTATTTCCTCCCTGAAG



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WI-21475b	117	A T ---	---	TAGCCCTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGTAGTGGGCTCCAAACCCAGGCTTCCTC/TATCTTGTCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGCAGTGGCTCTTGGAGAAGGCAAAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTCCCGTTCTCCACCCTATTCTCCTCCCTGAAG
WI-20893d	207	A G ---	---	TGTTTGTGTTCCAGCCACATCTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTAAAGTGTCTACTGAGGAATACAATCATTTGTACGTAAAGTTATCACCAGCACTCC AGCGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTC/A/GJACATAACATTTGGTAGAGTAAACAACAACCAAGCCCTAAATG
WI-20893c	179	T C ---	---	TGTTTGTGTTCCAGCCACATCTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTAAAGTGTCTACTGAGGAATACAATCATTTGTACGTAAAGTTATCACCAGCACTCC AGCGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCAT/CJ/TTCTCTCTTTTACAATGC AGTTTCAACATAACATTTGGTAGAGTAAACAACAACCAAGCCCTAAATG
WI-19941c	71	C G ---	---	GAGCTCAAGGGAAGACCCCTTACCCAGATAGGACTAACTGGAGGGGTGGAAGGAAACAAGGTGAAA GGTAT/C/GJGGTCTGTGAGACAAAAGCAGGGGGGCTGAGAACACAGAGCAAGGTGGTGTGGAG GGAGCACAGCAGGGTGCAGGAAGGAGATGGGGGACATTTCTTATTCAGTGCATGTCCCTTAAAT AACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAGCAAGGCG
WI-21552b	166	C A ---	---	TGGGTACATGGACAGATGTATATGTTTATGGGTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAATGCGATCTCCTTCACCTCAAGCATTTATCCATAGTGTACAAAGAA TCCAAGTATCTCTTGATTTTAAATGTATC/AJAAATTAATTTATTTGAATTTAGTTACCCCA ATTGTCTATCAAATATTCATCTTATTCATCTTTGTAACTATTTTGTGTA
WI-21552a	66	G A ---	---	TGGGTACATGGACAGATGTATATGTTTATGGGTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAATGCGATCTCCTTCACCTCAAGCATTTATCCATAGTGTACAAAG AATCCAAGTATCTCTTGATTTTAAATGTATC/AJAAATTAATTTATTTGAATTTAGTTACCCCA TTGTGCTATCAAATATTCATCTTATTCATCTTTGTAACTATTTTGTGTA
WI-21512	54	C G ---	---	TCCCTGCTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAATATTTCTGT/C/JTAGAGAGGGA AAGAGCTGGTGGCTGCTCTGGAGGGAACGTCAGGTCGGGGAAGGCACTCGTGGTCTGTGATCTGTC TCAGTGATGGGAGGTCTCCACTGCCCCACAGGAGCCTCGGGGCCAGAGATGAGAAATATGCTGTAA TCCAGTACAGGGGCTGCGTGTGGGGTCCCCAACAGCTCCTTCTTTGGGGG
WI-21513b	192	G A ---	---	CACATAGTTTCTCAAGAAGAGGATGAACCTGAACCTCTAAGGCGAGGACAAAGCAACTTTCATT ATTCTAGTTTAGACCAGATCTTTAATTTTATATTTCTCTTTAATACTGTCAAAATACACCAATA CTTAGAGGAAAATATTCACAGTATACCAAAACATTTAAGATAAAGAGGCGAGTGTAA/G/JAGTAG TATTCTCTACATACCACAGTATACAATGATGCTCTCTCTGAGGTTTAGGAAC

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WI- 21514b	133 C T ---			TTGAACCTCTGAAGGTGGCTTATGTCTGACTCCTCTCTTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGATATCTCAACATTACAAACCCCACTTCAAGGAAGGAGCAGCATACCATTGGAGC[C /T]ACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTGAITTTGCAAGGGTCATAAGGAACT
WI- 21514a	100 A G ---			TTGAACCTCTGAAGGTGGCTTATGTCTGACTCCTCTCTTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGATATCTCAACATTACAAACCCCACTTCAAGGAAGGAGCAGCATACCATTGGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTGAITTTGCAAGGGTCATAAGGAACT
WI-22020	27 C G ---			ATGAACATGTTGCAAGTGGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCATCTACCTGTATGAGGGTACTT
WI- 19576a	113 A G ---			TTTCATCGGTTCTTAATACAGTACAATCCTTTTGTGAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATT[C/A/G]TCTAGTTCAAGTATTAGT CACAGAAATTAACATCTGCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCCACGGGGA G
WI- 21695a	141 A C ---			ATACACAGGCCACAATGCAGGATGGAAGGAGTGGGCACTTGAAGTGACTACACATGCGCAATA AGCAGCCTATCTCTTACCACCAAGAACTTCTTGGGGCATGTGATGGCCAGACCCCTTTCCAA GGGAATA[C/G]TACTACACTAAGCTACACTGTACTGTGAGAGTCATGGTGAACAAGGCCACAGGC AGTGGAGGAAATGTGATGACTTCACTGTTCAGANTTCTAAGGCCAGCAT
WI- 21574a	235 C T ---			AAACCCAGAAATTTAGGTACTTTTGATTATGAGGAACCTCACTATAGGAAGCAACTTATGAGTG TGTAATATTGATCTAGCAGCAACTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTAATGTCCTCAGAGTCACTAGGAGGCCATT GGGCAGGCCAGGGAACCTTACTGCCTACTTCTT[C/G]TGTCTGTCAGGTGGGA
WI- 21644c	151 T A ---			TGACTGCCAAGATTTAGGCCCCAACTTAGGAGCAAGGGTCACCTTAACCTTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTACCATANTATTAAACAGACTCAAGGTACATACAAGCTTG TTTCATAAATAAGGGA[T/A]TTCAATCAAGATCCATGGAATGATGCAGTTTAAATGTTCTCAGC TTGCCTACTGACCACCTTCTCTTTCTAAATATGGCAACAGCACAGCAAGTC
WI- 21614b	55 G A ---			TGCTTTAACCTCAAAAGTCCAAATAAACATATAGACATTTTGANTATAGCTATC[G/A]TTTTAACA AACCTCATTATGATCACTGTTCGAATTTCACTCACCTAAATACGGAACCATGACTATTAAATAACA TTTACTGTCTGTGGGTTTGTGGGACTGAACATTAAACATACGTGATTTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI- 21615b	151 C T ---			GACCGAGAAAAAACTGCAAGGCATATGATGTTTGTGCAAGTATCACATGACTATTTCAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTCATACATATTAAAGATAAGGATGGACT CTTTCAGTGATATTAT[C/T]AGGACACAAATCGACGGATGTAATCTATTGANTTATACCATAGGCC TATTCTATATTGGCCAAAGGGAAGGTAGGATGGGTACTGTGGAAACGGA

WI-21981	61 T A ---	---	TGTCATCTCATTCTGGAGAAATCATAGATGTGGCAGAAAATACATATTCCTTGAAGAAAAAAATTAJGTCTCCCTTATGGGTACTGTGATTTCAATAGGGTGGGATAGTACATGACAACATGCATGGGATAGA CACTCTGTTCTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGTTAAATTGG
WI-21660	120 C T ---	---	TCCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAAACAGATACGGGTGAACACGCCTCTCCACTGCTTACTGTGTGTACCAAGAGGCAGAAAGCAGCTCACCCAAAGCCTAACCTGGCC[C/T]GTCTTTTTCAG GCTTCTCAGGATGCCACAGCACATACTGGGAACTGGGATGCAGGGAGAGACAGGGTCTGTCTTC AGGAGGGTCACAGC
WI-19105c	211 C T ---	---	TGGAAAGTAGCCCTTCTGGACAGAAAAGAATATTTGGTCCATGTGGTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTCTT GTCTGTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGGATCTCCCC ACAACTTC[C/T]TCCAGGGGCAGGATTCCACCCAGGGCCAGGGTGCCCCG
WI-19105a	33 T C ---	---	TGAAAGTAGCCCTTCTGGACAGAAAAGAATATTT[C]GTGGTCCATGTGGTTGAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTC CTTGTCTGAGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGGATCTC CCCACAACCTCTCCAGGGCAGGATTCCACCCAGGGCCAGGGTGCCCCG
WI-21760c	81 C A ---	---	CAAACTAGTCACTCTACTGATGCAAAATGATTTGGAGGTGCTTCTAGCTTTACAATAAGNGGAGG GACCTCTGACTGCA[C/A]CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---	CAAACTAGTCACTCTACTGATGCAAAATGATTTGG[A/G]GGTGTCTTCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCACCCCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---	TCTGCCATATTGTTCCAGCACCACCTATTACTGTTATTTCTCTTTGAGGAAAAACAGGNATTAAG AAATCTGGTTTGAATTTCCATGATGCCTAACCTATGGTTAAAAATCCTTTTCTTACCAAAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGAGAGACTGAGATATGTTGCAGAAAATTTATCTCTAC[T/C] AGAGACAATTCATAGTTCATAATCTTTCAGGGTTGTCTTACITGGGGGGC
WI-20934a	72 T G ---	---	CCAACATGCAACATAGTCTTCATTCTTAAAAAGTACATAGTAAAGTATGAAAAACATTTGTATTCA GAGAA[T/G]TCTAAGACAAATGGTCAAAATATTCAAATGGCCTGGCAGTGGTAATTCAGCAGAC AAACAGCATGAGAAAAAGGCCGGGAGACAGTAATAAATACGTGCCCATTTGCAATGAGTTACCCAATC AAGCCCTTTTACCTCCTTAAGATGGCAGATTAGAAGACCCCTTTCCTCCAGGAGA
WI-21561	55 T G ---	---	TTTCCATTTTATCAGCCGGGCCATCAGAACAAATAGCATCTATACCTTCGAAACCTT/GJCCTCTTAAC CTCTCCAGGCAAGAAAGGAAAGTATGATATTAATTCCTCAGAAATGGTGGGATCTCAAGACTT TTTAGAAAGTGCTTATTAAGTATAAGAGGCTTGAATATAATGATGATAAATGGTAGCCTTTCTGGA ATAATTTTGTGTAATCTGTTTAAAAAGATTTTTTGGATGCATTGTCCCCA

[illegible]

WI-22082L	67 C T ---			CAGGACTTGGTTTGGTGTCCCAACTGCACATAAATGTCCCTTTTGTGAGTTATGGTTGTGIG[C /T]GTTTCCCTTTTGCATAAGAAATATGTCATTTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG AGGGTACACGGGGCTCCGCTCAGTCCCGCCGGAAGGACGTATTCGCTGAACGTGGGACGAGTCTACTC CTCCCCACAGGAGGCCACGATTTCAAATCTCTTTGTGCAACCTCT
WI-20993	139 A G ---			AACACAACTCCATGCTTTCAAGATTCCACACCCAGATACTAAGACATATTAAAAATTTACAGCAAT TAAACAGTGTAAGTTGGTACAAATACACATATAGCAATGATACAAATTAGGGGAAAAAACCCCTGG GCTTCT[AG]TAAACAGTGAGTATACATTAAAGACAGTATTGCAGAAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCTATTTCAAGGTCTTCCTAGCTCATCCACACATCACC
WI-21723b	125 A G ---			AAGCGATTTTATTAAATTGATTTGGACATACCTGTAGGTCAATAATATTTCTGAAGATAACAATTA TGGACITTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCA[AG]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82 G A ---			AAGCGATTTTATTAAATTGATTTGGACATACCTGTAGGTCAATAATATTTCTGAAGATAACAATTA TGGACITTTAAAGCTC[AG]ACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99 T G ---			CAACAGATGCTTGAGCCAAAAAGCAACATAGGCAGAAATACAAATTGAGAAATATCTTCATGTTTC AACCTTTAATCTGACTTGCCTTTTACTATCCTT[AG]GCCCCATTTCTTAATCTCTTTGCTTACAA TATATTACCTTCTAGGTATCACCTCATCCTATAGGAATGCCCTTCTAGTTTAAATGTCCTGCCCAAAACA ATACTAACCCATTGAAGGATAACTATGGAAACCTTTAAATGGGACAGTGGG
WI-21006a	106 A G ---			TGACAGATCACACCCACATTTGTTTGTAACTTTTCTCCTTCAAGAGTCACCCTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACATGTGCACACAC[AG]AGAGGCAAGTACAAAAATGTAAACC CCACCAAAGTGCATGTGAATGAAAGTGCAAAAAGGCTTCATTTGCAAACTCTGAGGATCATTTCTCT CTGCTTCAGGAAATAAACAGAAAGGTCCTAACTGCCCCTAGGCT
WI-21761b	138 C G ---			CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCTGCTTGGAAATAACTGAAAAAGATTTCAT TTTCTCTTTGTGTACAAAGGATTCAAAATATTTACATCTTCTCTGCGAGTTAAACGTGCCGTGG CTC/G]CAATACACACCAAGCCAAAGCGTAACCTTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166 G A ---			AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTGTATTCCTCCATGAATTAAGCTGTGTGCTCACTTGTTTACATAA CTCAGGCCACCCCTGAAATATCTGCTAGTGGG[AG]AATTTACAACCCACTGACCATCTCAGCTCAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAAATAGGCATGGGCAAT

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WI-21079a	50 G A ---			AATGAAATGCCACCCAGAGGTTAACAGCTGCCATGCATGCAACTGTGTG G JCGCAAAATCAAGT TGTTTTAATACCAAGTGCAGCTTTGATTCCTCCATGAATTAAGCTGTGTTGCTCAGCTGTTTACA TAACTCAGGCAACCTGAAATATCTGCTAGTGGGAAATTAACACCCACTGACCATCTCAGCTCAA GCCAGATGACTATCACTTACATCTGCGCAGGGTAATAGGCATGGCAAT
WI-22129a	45 T G ---			TCTGTAGATTTAGCCATGCCATATATTTAACTTTAAGGAAAGT G JTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCAATAAGTAGCTTAACAGTTAACTTAAGCTTATACCTTATATTTA AATGTTAGCAATCTCTACTACATTTTCAATATAAATAATTTGGTGCAAATCCAGNAAAGGGCA TTAACAAACATGGGACTGATCCTGGGGCTTCCACCTGACTAAGTTT
WI-21941	79 A G ---			TGGAGTTAAGTGGGGCTCTGCTATTTCCCCCAAGAGGACTCGGAAGATGTTGATTCAGGGCAGAGT GAGGGGCAGAC A G GGATGAGGCTCTTCTGTAAAGTCCACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGTTGGAGCTCACCAGAGAGGCTCAGTGCATTTGACCCACACACCCACTCACC CAGCACAGGCACACGAGGACACGACACACACGNTGCACTCACCACGC
WI-18916b	42 C T ---			AATGGCATCCCTGTCGATACCAACATCTTCAGCAGCTCAGC C TGGCTCCCACCTTCTTGGTACCC GGTTAACTGCCAGGNGGTGACAGTGATGCCAGGGCTGCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-18916a	35 G C ---			AATGGCATCCCTGTCGATACCAACATCTTCAGCA G C TACGCCGGCTTCCCACCTCTTGGTACCC GGTTAACTGCCAGGNGGTGACAGTGATGCCAGGGCTGCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-19828c	200 A G ---			TTCCCTTCTCCCCAAGAGTGGCAGAAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTAGCTAGCTAGTCCAGGNCCTCTGGCCCCAATCTGGGTTCTCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTTCTCTGACCTCACCACCACCCAAAAT A G  C TTTTAATTTCTGAAAAGAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47 C T ---			CACAAGAGTCTGTACAACCTTAGGGACACAGCCCTGGCCCTGCCC C T A GCTGCATGCCACCCTC ATATCCCACCCCATCCAGCCTCTGCCCCGACACCCCGAGGCTCCCTGCTCTGGTTGAAGTATTT CTCCAAGGCAGGAATGAGTCTTGATCCAAACACAGCATCT
WI-19860	51 C G ---			TTGACCTAAGCCTAGCATAAAATAGCTAAGTAGAATGTTTCCAAAGATG C G CTGCATCAGTAT CTCCCATCCACATAATTTCTGTTGATTTTGCCATTACCCCATAAATGGTGGGATCTACCTCCCCT CCTTGCAATTTGAGCTGGNCTCTGATCCTGCTCTAAGGATCTGAAGCC
WI-19889b	80 C T ---			ACCCAGCTCCTTACCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAAACTGCAGGGCAAG AGGAGTGAGGGG C T TACAGCATTTATTTCCCTCTTTCACTCCCTGTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCTTGGCCACACAGTCGTAACCTATTCG

WI-19891c	172 C G ---	---	---	TGTTGGTCTGAGAAATTCACAGCTTACTACAAAGGAAGCTGAGAAATGCTTGGTGGCCCTCCCCCCCCG ACTCCTCTGCTGGGAAACGTGGCTTTGNCTCCAGACACAGTGTGAGATGCCAGCTCTCCTCAGCGG AGTCCCGATCCCTCAATTTGCCATCTGTCTGACTC/GCGTCTCCCGGGCGTGGGGCGTGTCTGT CAGGCAGGGGGGGAGGAAGGAAGGAGATCCAGGCTGTCTG
WI-20155a	81 C T ---	---	---	GCACCTGTAGGGGTAGCTTCCATGGTTCTCCAGCAGGGCTGTACATTACCTTAGGCTGAACAT TCCCTTGGGGGGC/TGCAAAAC.TGCTTTGAGGAAATNTCCAGGAGGAATAAAC TAGAAGACGC ACCTGCTATTTCCACCATACTATGGAGAATACAGCTAATGAAGTGTGGCAGAGCTTGGCCGTGTGA GTGCCCCAGGGTAAAGTCTCTCTCTCCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91 T G ---	---	---	AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCGTCAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCA/T/GJACACCAGGATTTATACACGGTGGCAGCGGTATAGGCA CGATGATACAAATATAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGAAGGATGCT GGGTGATCTGTTTCCCGCAGAGGGCTGGGAGGCGGGGTTGGTGGGA
WI-20270a	53 G A ---	---	---	AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCG/TGATCAGTGTAC AATACATTCATGTCCAGGATAAGGAGCATACACCAGGATTTATACACGGTGGCAGCGGTATAGGCA CGATGATACAAATATAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGAAGGATGCT GGGTGATCTGTTTCCCGCAGAGGGCTGGGAGGCGGGGTTGGTGGGA
WI-20622	130 T C ---	---	---	CCACTTCAATATTTACAAATGCTCAGCAGCAATATGAAAGCTTCAACACTTCCCTTTGTA ACTTGCTGCAATAAATGCAACTTAAACAAACATACAAATTTCTCTGTATCTTAAAGTTGAA/T/C TACTAATTTTATGATGTACTCATATTTTATTCATATACITTTAATGACATCATTTGCCAATACATA CATATTTCTNTAACTTTATTTTACAATAAGCCAAACATCTGTCATGCAG
WI-20768b	190 C T ---	---	---	TTCCCACTCAAACTCCCAACCTTCTCTGGAAGGCGGGCTAACAGGACCTCTGCTGCTGCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTCTGTATATCACCACTCTA CAGGAGAGGTCTATTTCTGGGGCACCCAGAGNITCAGCACACATACTGCTGGGAC/T/CAGGGACTC GTAATTCGCTTGGTCCAACTCTCTATGGGGTTTAGCTGCCCTCATTC
WI-20768a	71 C T ---	---	---	TTCCCACTCAAACTCCCAACCTTCTCTGGAAGGCGGGCTAACAGGACCTCTGCTGCTGCTGC TCA/C/T/GACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTCTGTATATCACCACT CTACAGGAGAGGTCTATTTCTGGGGACCCAGAGNITCAGCACACATACTGCTGGGAACAGGGACTC GTAATTCGCTTGGTCCAACTCTCTATGGGGTTTAGCTGCCCTCATTC
WI-21909	153 A T ---	---	---	TGTTTGTCTTGTGCCAGGTACTCTACTGCTTTACATAAATTAICTCATTTCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAATAGGATATTTGGTGCATCTTTAAAGAAA TGCTTTAATACATACCAAAG/TJAGTGGAAATCAATAGAATAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCCTAAATTTATATTTCTATGTATGGAAAG

WI-22202	128 A G ---	---	TGTTGCTTTGGTTGTTGCTTCTGGAAACATATTGGAACACATTGTTTTCATAAGCTGTCTGACAGT GGACAATCCCATCCATCTTCAGGCCCTTTTAAATAGGTCATTATGAAATCTGAATTTCTTGA/GJTAAAT ACTCTGGTGCAATTCATCTGCAAAAGCAACTGGCACAAACCACCTCTGCGGGTGACGCTCTCGG AGAACATCTAATATTGAGTCTAGTCTGTGCGGGAACCTTCTCCAGCTCAC
WI-22189	70 C T ---	---	CCAAAGGATGAAATTTCCACATTTATTTTNCCTTTTATGTGAATAGAAAATGGCAGTGAAGTGTCTCTATG AACTGTGAGGCGAGGAATGGCATGGCGCTGCGGTACCAAGCTGGACGTTGTGCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109 T C ---	---	GGGAGGCATCATAGAAAAAACCCTCAGCCAGAGTTAGGACATTGTGATTCAGCCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCGCAGGCTCTGGTTGTC/GTTCAATTTGCAAAATAAACCCA GACCGGTCACTCTTTCAGTTCCCTCCAGCTCTATTTATTTATGATTTGCTCTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACCTCACTCCAAATGATGCAAAAG
WI-22290a	136 C T ---	---	GACGTCATCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTATGGGCCCTCTAAGCACCG GCCAGTAGTGGGAATGCCACATGCAATGGTGAGTGGGATCTGGGGGGTCAAGGACCTTGCTTTT C/GTTCCAATCTCTCTTCTAGCCAGAACTTTGCGAGAGCCCCCTTNNATTTCTCTCCCTCTATTCC CCTCCTTTCCCCAAATGTCTAAGGTCCCAATTCAGACGCCCTCCCG
WI-22292	53 A G ---	---	CCAGTGAAGGGTTACAGCCATAGTGAGGTTCCCCCATTTGCTCAGTACCAGA/G/GJTTTGAGTAC GGTCGTTAAAAAATACTTATCTGACCACAGTGGAAA
WI-22387	186 C T ---	---	ACCTTGACACACCTGCCATCGGTGCCATCTCTGGCTGGCACATCTATACCCACTCTGGCTCTGAAAG GCTTGTCAACCAAAAATGGCAGCTGGGGCTAAGGCATATTTAAACAAAGCTCCAAAGGACCCCTT TCACTGGGTCTAGCATCCAGCCTCTCTCTCAGCAAGGCAGGATTGGGTCT/GCTTGTGTTTCTG AACAGGGCCAGGGCAGCAAGGCATGCCATCACTGCGAGCACTCAACCCCT
WI-22395b	127 A G ---	---	GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTCATACAGAAATGGTCTTCTTGAATATTTT GTAGGATGGATGAATTGAAAGTGAATTAAGTCAAGATAAAGGGGGCAACTCTTTAAT/GJAAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	TTTATGGCTCTGAGTGCCCTTCAACCAGCTACACTTTACCTTGATCTATATAAAGTGTAAATTTAGAGT AAATACATTGGCTGTAAAGTCG/CJGATCAGGTGCTCTCCACCAAAAGCAAAACAAACTGCTGA AATGTGCAAGGTTTCTCAGTG
WI-22419b	67 T C ---	---	CCCTTCTGGACAGTTGCTTTATGTGTTCCAGACAATCAAGGNTGCCCTTCCAGGCACAGCCCCAGTGCTT /CJCTGGATGGCATCAGCACAGGCTCCCTGCCCCGGCCCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59 T C ---	---	ATTTTCCCCTTCTGTGTTTCTGTTTCCCCCTTTTGTGTCAGTAAATNAGCAATACACTGAT/CJTGGA ATCTGCATGATTAAATAACATTAAACAGTTCTATAAACACACCCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCCCTAACCGAATGCAAAATTAGGTATCCCTCAAAATTCACACA TTTCTCCTCTAGTT T



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WI-21763b	154 A G ---	---	CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGTAGTTCCCTCTTTAGGCTTCAAGA TAATTGTAATTCATCGCACCCAGATACITCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATTGAGCAGACATTGCTGTGCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-21763a	135 T C ---	---	CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGTAGTTCCCTCTTTAGGCTTCAAGA TAATTGTAATTCATCGCACCCAGATACITCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT T/CJGCTCTCCACAGCTGATTACAGACATTGCTGTGCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-22440	64 A C ---	---	CAGTCCATTTGAGTCCCCAGTCGAGGGTGCATTTCTCTTATCTTGTCTTAAAGCCACTTGGGTAGCJ TCCATTCAGCTCTGCACCTTCTCCAGTTTCTCATGTGAGAAGTCCCTGGAGGGAGGCTTCTCTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTNCCATTGTGTGACAATTTATTAGCTGGCATCCGAATACAGTAC TTCTTTT/CJGAAAAAATACACAATGGGAACGTGACA
WI-21965a	112 A G ---	---	CAGGTTCCACACAGAGGCTTTTATTCAGCCACTCAGGACCCCTGGCTTCTGTCTCCAAAGGCACCTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGGACCTCCCCACAGCCJAGJCCCCACAGGGTCTCTGT TCCCAAGTCTCTGATGGATTAGGCAAGACCTTCACACATTACCCCACTACCTGTGGAGAGGGGTC ATGAGGCAGCCTGTGTGGTCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTICA AACCACATGGTTTCTAGTCAGAAAGTCTCATGGACTTCTTCTCCTAAGCJGJGTCTCTATGATCAGAC CACCTCTAAATGTGGCTTTTACCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAGGAGCCCTGAGAAGAAATTTTACACAATATTGACTATACAGAG TCTTCAATTCCAAAAACAGTTAATAGTAACTTGGTGGCACATACAACATGCATTGAATACTCTGTAT TATTCAAGTAACTAAAT/CJAGGNTCCTGCATCATCTCTTICACA
WI-22250b	132 C T ---	---	ACTTGTCTCAGGCAGGCAATTTCTGGGATCTAACTAGAAATCCTTGAAAAACAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTGAGTGGGTATTATGGGGTCTCTGCCCTCTGGCTGTGTTATG[C/T] GGANCCAGGAGTGGAGAGCGGTGGAATAGACAGGGGAG
WI-22250a	89 G A ---	---	ACTTGTCTCAGGCAGGCAATTTCTGGGATCTAACTAGAAATCCTTGAAAAACAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTGAGTGGGTATTATGGGGTCTCTGCCCTCTGGCTGTGTTATG GGANCCAGGAGTGGAGAGCGGTGGAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGCCATCTCTCTCCAGACCTCCAGGCCACCCCTGGGGCCAGAGCACTCATGCCAGCAGCAC CTAGTGGCCCGAGTACGGACCCGCTGGCCAGGTCTCTGGCTCTCAGGACGTOCCAGCAAGTGGA GCCAGAGGTTTGTGGGACTCCAGCCAGGGGATAGGCCAGCCCAAGAACCTG[C/G]CJAGTGCTTC TTTGACGGGGCCCGCTGCTCAGCTGCTCTCTGGAGGTGAGGAAGGAGGT

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stSG1019 3	136 GA ---	---	---	GGAAACAATACTACCTAAGGACAAAATACTATTATAAAAAAAGCTCTTCTAGTGTATATTGTGTAA CACATTTCTGGAGCTGGTAGGAATAACCAATTTTATTTTCTGTAGTGCCATCTATACAAAACCTTTTAC T(G/A)TTTGAAACCTGAGATTTAAGTTGCAAACT
stSG1020 2c	143 GT ---	---	---	AAGCTAACTTAGGTGAATGGTGCCACTCAAAAGGTCTTTCCGAGGGAAGCTCAGTCCTGGCTGGCGAG AGTCAGCCTTGGTCACCTCATAACGGGGCTCCAAAGCTAAGCGTCAAGGAAGCAGTCCCACTGCTTCT CGCTGTCA(G/T)CAAGACCACAAAGGCAGATGCCACTGCTGTCTCTTCTTCTGTCTACTTTCT
stSG1020 9b	75 AG ---	---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTCAAAATAAACTAATTCCTCTTAAGATCCCACTTTAT TTTTA(G)CTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1020 9a	34 CT ---	---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATT(C/T)AAATAAACTAATTCCTCTTAAGATCCCACT TTATTTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29 TC ---	---	---	TACTAGACATGCAAAATGAGAAGATTACA(T/C)GTGAATATTTAAAGAAATTATATTTGTTTGACAT AATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTCTGA
stSG1025 2	108 AC ---	---	---	ATAGGTTTCAGGAACAATAATCATTAAATGGAATAAATGAGAAGAATTCCTTTATTTTGGACCAATTTT AGGCACCTAAGAGTTTCTTTCTCTCTTCCCTTTGATCA(C/A)GTGAAGATATGATAGGGAATTC AGAAATTTCTCTCTCTG
EST10915 0	123 AC ---	---	---	CTGTATTAAATTAAGAGGCACCTATTAAATGAGGGACGGGAAAAATCTACCTGTACACAAAAATTCGTAC TTTAACAGCATCTTCAATAAACCCTTAAAGGATAATGGTTACGATCATTTTAAAG(A/C)JATTTTAA GAACTGAGTTATTGGAC
EST11023 1	166 TA ---	---	---	TTTTTTGTTAAACCAACCCTGAAAGTTCCACATGTGAATATAGATACAAACAGTGAACAAAAAT ATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACAGTAAACAGCAGGGC AATTAGTCAATTAATAAAAAAATAGTACATGTTA(T/A)GTGTAATAAAATTAATTTACAAAGGCTTT TCCACTCGTGGATTGTATTCCTTTTGGAGGGGAGTAATCCTGG
EST14096 8	71 GC ---	---	---	GGGATGTATATTACAGATAACACAACTCACAATAATACCATCAGACATTGAAAACTAAGGCCATTCT GTGA(G/C)TTATTTTAAACCTTGGTGTTCACACATAATGATCTTAAAAAATAATGAATTACCAAA ACCAAGATTCTCTTCTAAATGAAAAATTTAATGCAGGTACAGGATAAATTTAGGGCTATATCTAATC TGAAG
EST22113 6c	125 CA ---	---	---	TGCAAAATTGTGAAGGCAGCAGGGGCCAACCCCTGGGACCTCATCTCTGTCTAGAAATGTGAGGTGCG CAGGGATGCTTAAGTCTTCTCTGGCAGAGACCCGAGGTGCAGAGATGATTCCTCA(C/A)CCCTTC TCTCAGGGTCTGTGAG
EST22555 7	60 GA ---	---	---	TCAAGCATGTGTAAAGGCACCTGCCCCGCCAGACCCCTTCTAATCTCTGCACACTGGAAGGT(G/A)AAA CCTGGGAGAGAGACACTCCCTCTCTAGCTTCTACCTGGGCCCTCCAAAGATGAGCATTCATC TTGGAGACCAAAATAAAAAAGGACAAAAGACCAGGGCTCAGAG

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EST22917 6	74 C T ---	---	---	GTAAACCTTGCAAAGCCATGCTAAATGGAAGCCTGACTGACCAGGGGCTCTTGGGCTCTCAATGCA ATAGAAAC/TTTGACATGGGGCCAAAGACTTCCAGACAAAGCACGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---	---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAACCCTCAGGCTGCTCCTACTCA/AV GTTGTGTTTGTAGCTCCTCCTCGCACACAGGAAGCTTGAATTTGGAGGCTCCAAGTCACTCTCCA GAGGGGAACCTTCAAAGAGGATCCAAACAGTGAAGCAGAAATCATGGGGCAAAGTC/AG/CTATGG GGCCAGACTGAGGTTGGAACACACAAAGCACTCCAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGACGGAGTAGCCAT
EST36745 3	56 A G ---	---	---	TGTGACCATACCAAACCTATGCAATAAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAATACAAAATGTGTATCTCCTGAGACACATTTATAAACATTTCTGGTATG T/ATTTATGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410c	201 A T ---	---	---	TGTGACCATACCAAACCTATGCAATAAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTCATAGCATTTTGGGA ATTTATGTGTGAATAAATACAAAATGTGTATCTCCTGAGACACATTTATAAACATTTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410b	139 G T ---	---	---	TGTGACCATACCAAACCTATGCAATAAAAGAAAAAATCCTCA/CT/TTTAAAAAACAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTCATAGCATTTT GGAAATTTATGGTTTGAATAAATACAAAATGTGTATCTCCTGAGACACATTTATAAACATTTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410a	48 C T ---	---	---	TATCGTGGGAAGTTCCAAACCTCATCTATGCTGCTTTTCTACTTGTCTAATATTGGATGCTTCTTGCCA GGCTC/CTTTAAATTGTGCTGAACCTGGGAAGAAACCTTCTACTCTCCACAAACCTGAA
STS- R42778	74 C T ---	---	---	CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGGTTTCTCCCGGGATGGTGAATAATGTTCCGGACCTAGATA/CT/GT/GACGA AGGTAGCACGACACTGTGAGTGCACTAA
UTR- 04350	125 C G ---	---	---	GAAATAAACTAAACTGCAAAGCAAATCACTGTTTAATAAGAAATGTTCTTCTGTTT/CJGACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGGAGCCAATGAGTCTCAGAAATGCGGGCAAA CTCCTCTGGAATAATGTAT
stSG1026 6	55 T C ---	---	---	GTATAATTCAGCATAAGCCCAAAGCCCTTTTAAATAACCAATACTATCATTTTATGAAATCTTTTACA AGA/T/GAAGCACAGTAGTACAATAATTAAGCACTCAAGTCTCCATTTAAGAGTTGACTATC
stSG1028 2	70 T G ---	---	---	CACTTTAGATATGAGGAAATGGTTTAAATGGACACAAAGAGTCAAGCCAGTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTGATATGCAAAATACAGCAAAATAATTTTTCACCTC/ATTTG TCAATGCCAATGCATTGAAAGGCCCAAGAAATGAGAAAAGGATAACAACTTTTGTATAAAAAGGTA AGAATTCCTGTGTG
stSG1031 0	128 C A ---	---	---	

stSG1033	116	T C	---	TTTAAAGCTACATGCTGAAAGAAATGATGCTGCTGATTGAAATAAAGGAAAGAAAGATGCAATTCGGG GCTCAAACCTGCTAGGAAGGCTAGACCTCAAACACCAACACCTCCATTCGATTCCTCTCTTTGG CTACTATGCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
1b	107	A T	---	TTTAAAGCTACATGCTGAAAGAAATGATGCTGCTGATTGAAATAAAGGAAAGAAAGATGCAATTCGGG GCTCAAACCTGCTAGGAAGGCTAGACCTCAAACACCAATTCACCTCCATGCAATTCCTCTCTTTGG CTACTATGCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
stSG1243	225	G A	---	ATTGGCAAAATGGGAAAATGACACCAATCATTTGATTACAGAAAATGGTTTTATAAATCCTCCTCTTG AAATTATGTTTCCAGGCCAGCATGGTAGCTTATGCTGCATCCAGCACTTCGGGAGGCCAAGGAGA AGGATGCTCTGAGCCCAAGGAGTTGACACCAAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATTTCTGTTG[A]AAAGTAATTCAGACCCAAAAGGAGGT
1a	60	G A	---	AACTGACGTATCACAGGGGCAAGTATCTGTGCATAAAATTTGAACCTAGTTTGTCTTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
stSG1345	54	T G	---	AACTGACGTATCACAGGGGCAAGTATCTGTGCATAAAATTTGAACCTAGTTTGTCTTCTTACGGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
stSG1385	117	T G	---	TTAATGTCATOCAGGGAGGGGCCAGGGATGGAGGGAGGGTTGAGGAGCGAGAGCGAGTATTTT TGGGTGGGATTCACCACCTTTCCCATGAAGAGGGGAGACTTGGTATTTTGT[G]TCAATCATTAAGAA GACAAAGGGTTGTTGAACCTGACCTCGGGGGGATAGACATGGGTATGGCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTCTGTCG
stSG139	69	T C	---	TCGCTCTCTTTCCAGTGTCTTCCAGAAAGCATCCCCATGATGTTGTGACCGCACAGCACATTTGTGTCT TTCGCTTTGAGCACTTGCACCTCTGGCTGGCTGCTGCCACTGATGTGACTGTCTTGTCTGCC
stSG1427	103	T C	---	GATCTGGTTCAGACAAAGGCTGATTCAGAGACTCCACGTGTCAAGGCTCTGTTTGTCAATCCCT TGGCTCCTCCACTCCAGTTTGGCTTCTGCTCAITCAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTACGTCCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
stSG1471	50	A G	---	CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTGTAGGTC[G]GCTCCCTTGCATGA AATGTGGGAGAGGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1483	44	T C	---	CAAAACCAAAATCCTTCCCACGATATATTACTATTTAGTCTAAGT[C]JTATAATTCAAAGTTGAGA ATGACGAATTCAGAATTTCTTCATACATAAATGCTTCTTCCCTTAGTTCTGAGATGGGTA
stSG1696	67	C G	---	CACACCCACAAGTTTCATGTCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACCAAGTGTGA [C/G]AATGTGGAGGATGCTGTTGACGCTGTAGTACTAATGCAGGAAACCCCAATGCAAAAGAGAA AATGCCTGA

stSG1847 b	95 G A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAAGAATTT AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCAAATGTGAAACCAAAATTAATAAATTAACCTGATCACTGTGCT TCAAACACAACCTG
stSG1847 a	49 C A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTAC[C/A]CTAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCGTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCAAATGTGAAACCAAAATTAATAAATTAACCTGATCACTGTGC TTCAAACACAACCTG
stSG1897 a	83 A G ---	---	CTTAATGCCCTTCTCTCTCTGACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACTT[A/G]GCCCAACCACTTCTCTCCCGGTCICCCCAAGATGACT
stSG2022 a	86 T C ---	---	TGCTTGAGGTTTCAAAATCTGAGATATCTATGGCAAGTTTATAAAAAGTACATTTGATCAAGGTACAA TTTTTAACATTAAATACAT[C/A]TTCCATAATCTCATCTATTTAACATTAAACACAGGCCCTTTGTTGT TGTTATTTTCTCCCTACAATATTCCTGACTCTGTAGGACAGTGGGCTCAGTTGGGGGTTGAC T
stSG2076	104 C G ---	---	AAACGTTGTCCAAAATTGTGTTCAAGTTTCAAGATATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAACACTTAAGAAATATTTTGACATT[C/G]ACATCAGTGGGGCATTTT
stSG2108 c	71 A G ---	---	TTGAGCAACAATGATTGCGGAATTGGGCAGCTCCAAACCAAAATGATTGAGGGCTCCACAGAGA GAGC[A/G]TAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTGTTGTTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTTGGGCTGTGCTGA
stSG2108 a	49 T C ---	---	TTGAGCAACAATGATTGCGGAATTGGGCAGCTCCAAACCAAAATGATT[C/G]GAGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTGTTGTTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTTGGGCTGTGCTGA
stSG2141 b	173 A G ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTCTATTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCACTGGCATGGCGATGGTGCAGGTGGGT GCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[A/G]AAGTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATCTTGTTGCTCTG
stSG2141 a	113 C T ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTCTATTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCACTGG[C/T]ATGGCGATGGTGCAGGTG GGTGCAGTTCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGTTCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATCTTGTTGCTCTG

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stSG2148	50	A G ---				TGGAAACAACCGGCTATAGTCTGAGTCATATTTTATAGACCGTGATTTTC[AG]JAAAGAAACAATAA ATGTGGATTAGAAAGGAAACATCCATTACTGTATTTTCGATACCTTGTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68	C T ---				CTCAATGAGGACTCCATCAGCCAAAGCGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGCT [C/]TGCCGCGTGTACTCAGCTAATGCTACCGGGTGGAGCGCACACCGAGCCAGCCACCTTTTCCAT ACCTGGCAGAGGGAAGGAGTGGAAGGAACA
stSG2189	41	C T ---				CAAGTGTGAAGCTGGGATTGAGCCTGATATTCACACTA[C/]TCTACATTCCCTCCAGTATAATA GGAACATCATCGCTAACTTTGAGCACTTAGTGTTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTGCCAAC
stSG2200	49	T C ---				TGTTGATGACCATAGAGGATGCAAAGCTCCGGGCTGGTTCTGTATGATG[T/]CJTATATTTATGTAT AATGCTTAACCTGATGATACCCAAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85	G T ---				CATTTCTGCCTCCTGCTTCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAG[G/]TAGAGCATCTCTCAGCCCTGGAAGACAGTGTGGGAGCTTCAGCT
stSG2257	65	A C ---				TCAGTGATTGTAGGAGCTGGCTAAGTCATGCTAAACTCTGTGAGGCAAGGCTATCAGAAGGGCAG[A/ C/]GTGCAGGAACCTCGCCAAAGCACTGGGCTGCTCTCAGGCAGAAITTTCTTCCT
stSG2306	67	A G ---				GTCATCAGCGTAGAGTCACTGGTATAAACAACACAGTACTATATGATATTTGGGAACATATTTTACA [A/G]TATGCTCCCATTTGGTTTCCAAACTGATACAACCATGAGGTGAACACTTTTCACTGTTTCACAG TTCTCCAGAGA
stSG2334	70	T G ---				GAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAAAAATCCCCGCAAAAAACA AAAA[T/]GTTCAGTGGAGGGGCTGTGGGAGGGTGAATG
stSG2339	63	T C ---				AGAGCAGAATGGTGAATCAACAAGACCTCAAATTTGCTTGAAGTAACTGCTGTCAC[T/]C] GTTCTCAGAGTCACCATTAACGGTGACTG[T/]CTATTTCTGGCTGTGCTTCTCTATTCATCA
stSG2465	76	C T ---				CAAGACTAAGAAGCCGACCCGAGTGGTCCCACTCAAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA[C/]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTTCAAAGTGTGGGTATGCA
stSG2549	140	T C ---				TTGCAGGCTTGTATTCACAAATAACAAAGTCATGTATAGAGAATGTGAAATGATACTTGAAACCCAA GATATATAAAATATTGAAGTCATTTATGCCCTTTTGTAGTACTGGTTAAATATGCAAGCAGCTAAAG GAATAT[T/]TACACCACCCACCCCTTTTAACT
stSG2577	123	T G ---				AATTGCCAAATGGAAATTTCCAGAGGATTTTATAGACCAACTTTGCCCTGTGCTATCCCAAGTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGCA[T/]GGAACAATC CCGGCCCCAGATTAAATTAT
b	123	T G ---				

stSG2577	121	CT	---			AATTGCCAAATGGAAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTGTCATCCAGTTGGT CCCAATATAGGCTTCTGCAAGAAAGAGATCAATGCCGAACCGAAGCTGTGAAG[C/T]ATGAACAATC CCGGCCAGATTAAATTAT
stSG2700	58	GA	---			ATCTCTGACTGCTTTAGTGGGAAAGGAATCAATTATTAAGAACTGTCCGGCCCG[G/A]AGTCAC TCAGCGTTGGGGAAATAAACCACTGTCCAGAGAGAGGAAGGCTACTTGAGCCGGACACCA
stSG2724	101	TG	---			AAACAAGCTTTGTCAITTTCCACTACATTTTGTGTGCTTTATATTAATTTGCAATGCTATAAT TTAATACTTATATCCAAITGCTTGCAATAATCA[T/G]TTTTTTTAACTCGGGGTGTGAAAGAAC
stSG2776	65	GA	---			GTGGCCGATCTTTACTTTCCAGAAAAGGCGGTAAATAAAAACCTGTAGAAAAGTCTCGAATATGC[G/ AJATTTGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGACACTGCTGGCCCAACCACAAAA ATATCCACTAATCCCGAATATAGTAACCTGTCTTGCCGAATG
stSG2791	109	GT	---			AAGGAAAGGTGGAGGGAAGAAAGGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTC TATTATACCTCTGAACGTAACCTAGCAATTTTAATAAATATTT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGGTGAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
stSG2791	100	AG	---			AAGGAAAGGTGGAGGGAAGAAAGGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTC TATTATACCTCTGAACGTAACCTAGCAATTTTAATAAATATTT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGGTGAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
stSG2826	85	CT	---			CCGCAATTTCAACACACATCTATGAAAACCTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAACAA[C/T]GAACAAAATAAAGAAAGAAACCCATGAAATGCCCAGGTTTA ATTTTTTTCC
stSG2850	88	GA	---			ATGGGTGCATTGTAAAAGGCAAAATTAATACITTTTCAGGCAGGGGCTGGCAAAATTTAATGAGCTGA TGTGTCCTCAAGGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCTCTCCCAT
stSG3031	71	TC	---			ATACTACGGGGGCTGAAGGGCAATGTGAAGAGTGAAGTCAAGTCCCTGGCATTTTCTGTGGTGTGAGC AAATTCGGCCCTTTATTTTAAATGATCCAGACATCTGGGCAGCATAGCT
stSG3058	81	GA	---			GTCCCAACTCTCTCTCTTTAGAGAAAACCTGTGATTACCTCAACTTGAATAIGAAAACGTGATTG AAAAAGTCAAAAC[G/A]TGAAGAAGCATCAAGCCAAAAGGCAAAACTGGCTGAGGC
stSG3092	94	TG	---			CAGCATCTCCAGAACATTCCTAGAACTGAACCATTCCTGTCACTATTGAAAAACAAGCCAAAGTTC CAAAATCCAAAATAATAATGAACGTGC[T/G]GATAAACATTCCTTCTTATGGTCCAGCCCCCTACTTT AGTT
stSG3230	95	AG	---			AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGGTGGGAATGAATGCGAGATACGAGCACCTG CATCTTTAGTCAATTGTCAGTGGAGTC[A/G]TGGGGTGTCTAAGTGTCTGAACTGAAGTAG
stSG3245	160	GC	---			ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGCCC CAGGTATGTGAGAGGCCAGTGGGGGTGGCCACTTGGTGTCTTACCAACCCCTGCCATCCAGTCTG GCCCAAGTACCTACCTGGGAGGT[G/C]TGTACTTGGCTTAAGTACTTCATGCTTTAT



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stSG3265	42 T C ---			AGGTGAAATGAGTTACTAAATGTAGCATTTATTTATAAGGAA[T/C]GCATTGTGTAATAGTTTCTCAG TTTTCAATTATGGAAGATGATGATTTAGCCACACATTGATGATGTTTCTAAATAACACAATCGAC AGGACTGTCTGTTTCAATGAGGACAGCTTTTCAGGGCAATGGATTTCTTGATAATGCTAA ATCTGCTTGTGAGCTGAATTTCTGGGCTTTATGTGGCAGTGTGGTAAAAA
stSG3269 b	141 C T ---			TGTACTACTGTGTCATCCTATCCATTCCCTCCCTGAGCCTGGAGCTGCTTCCAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA[C/T]TGATAGTCCCAAGTCCCTGACACATTTTCTTCTAAGAACT
stSG3269 a	24 A G ---			TGTACTACTGTGTCATCCTATCC[A/G]TTCCTTCCCTGAGCCTGGAGCTGCTTCCAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAACT
stSG3284	130 C T ---			TTAACTCAAGAACTTTCAGTTACAGGAAGATTATCTAATATTAAATGACTAAATTACAAAAAGC ATAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCAGCTCAGACTTCCCCA[C/T] TCCCTAACTTTTGTTAATTGCTGTAATGGGACATTTGTTGTTTGATCTACCC
stSG3292	99 A T ---			GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAAATATCTAA[A/T]TACAAATCAATAGCATTTTCTTAACCTCAA TAAATGTCATATCTTTAGCTCTCACT[C/A]CCAGTGTATCCATTTTCCCGAGCCGTAGAGCTTTTCTG TTTCTGTAGATTTGCCCTGCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTCGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCAGTCTTCATTTCTTTAA
stSG3323	26 C A ---			GATCCCCAGTATTATTTCTAAATGAACTTGTTTGTGGAAATAAAAAATCTGAGGACCCTCAGAG GG[C/T]ATAAGGGAACCCCTTTTGTCTTAGTTCATAAGGACTTTCT
stSG3369	69 C T ---			CAAGACTGTAAGAACGTAGGCTTTGTGAGAGTGAAGGAAGGATGCTCGAATTTGCCAGGACTCAGG CTTCAGCTTCACAATCCCGAGGAAAGGAATGACATTTCCAACTGTACCTTTGTAGC[G/T]CTGGGT CAAAGTCTAAAGAGGACAAATAAATAGAGACT
stSG3398	125 G T ---			TCCTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG[A/G]CTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGCTGGCCTGCAGGACAAGTCACCATGCCTA CCTAAGTTTTGTAGAGACAG
stSG3416 a	43 A G ---			GTAAGACAAAGGTTTGTATGTTGACCAGGCTGGTCTTGAATCCTTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAAGTTGCTGATATTACAGGTGTAGCCACTGCCCCCGCGACTTTTAAACTGAAT GTTGAAATCATCTGCTCTTTGCTGGGTAACACTGA[T/A]CAAGTTGCTTAACCTTTGTGAAACCCAC TTTCTTATCTGTAAACAAATGGACAAACAGAACTTTTCTCTTCTCTCTC
stSG3424	173 T A ---			GTTCATGTTAAAGATTAGAAAGCTGTGGATGTGAGGGGTGAGGTGATGGAGGCGCTCACAGA ATGAGTGGCAGAGAGGGCCCTT[A/G]AAATAGCTTACTCTGTTTCTCTATC
stSG3436	88 T A ---			

stSG3463	103 C T ---	---	---	GATACAGAAGATAGTGGTATGGATGGATAGTGAAGGACAAAATAATACAAATATATTTATTG AAATAACAAAAATGCATACACAGCTCAATGGGTAC[C]/TJGGAAACAACTTGCTTGACTATATTA CTGA
stSG3491 b	71 G A ---	---	---	CAAGATACCTCATTGTCTAAGTAGTGCAGTGTGGCAAAATATTTCTCACGAACAAGGACGATTTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAACTCTCTAATCTTTACTGGCACCTGTGGATTTCTATTAAACATCAATTTATCTTCTGTGATG ACAGAAAAATAAGTTAAC
stSG3523	33 C T ---	---	---	TAGCCATCTTACTCTAGTCTTTTGGGTTTTC[C]/TGCCATATATGTGTACAAAACACACACACACC CCTAATCTCTCAATGCTCTTGGCATAAGTTTATCTCTTACTGGTCTC
stSG3536	213 A G ---	---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAAACCAAAATACAGAATGGCTTC TGTGATCTGGCCTTGTGAAACGCATCTCACTGTCATTTCTATTGTTTATAATTTGTTAAATGAGCTTG TGCACCATTAG[A/G]TCCTGCTGGGTGTTCTCAGTCCCTTGCCATGAAGTATG
stSG3583	112 G A ---	---	---	GAAAAAGCTTAACATACGATCCATGTGCAACCCCAACAGGATCTACGAACCTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586 a	60 G C ---	---	---	CCTAGTAACATAGTAGACCTCGTCTCTACTAAAAATTTAAAAATCAGGTGTGGTGTG[G/C]ACG CCTGTAGTCCCTACTTGGAGGCTGAAGTAGGAGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTT[GAGACTGTTTCAAAA
stSG3589	101 T C ---	---	---	ATATAGTGTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAAGGCAAAAAAAGT GTATATACCCCTGGCACAAAAACCCCAATGA[T/C]CCTATTTCCAAAGATGTATCCAGATGAAA GTATCCAACAACAAAAAGCTATATACAC
stSG3590 a	70 A T ---	---	---	GAGAGATGAGCTATTATTCTTTTACTTAATGAAGATGAAGAAATGATCTTCTGTTCTAAAAAAA AA[A]/TJTTCTCIGATGTCCTTGACCCGTGAGGAACACATTCAGTTTCTACACT
stSG3619	78 A C ---	---	---	CAGTGAGACTTCTCATTTTATAGCAAAATACATTTTTCAGCTTAAATTTTCTTGAATTCATATACGCT TCTGTCAATTT[A/C]AACAACTTCCAGAGAAAACTGGGCTCTATATATTTAAG
stSG3644	40 T C ---	---	---	ACATATGTAAGTCCATTAGTAGCCATATTTAGGATGAGAT[C/G]GATTGAGAGGATGAACCAAGG ATCGGTAATAATCATTATGAATAATAAGTTATCTGGGGAAACGGCCATTTGTCCAACATTTACTAA GTGCCCTACTA
stSG3646 c	70 G A ---	---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAATATGTCTTACT GGT[G/A]ATATAACTTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55 A G ---	---	CTCATAATTAGATTGAGATTGTGCAATTTGGCAAGAATATATGATGATAACAATAA/GJATGTCCTT ACTGGTGATATTAACCTTTGATACCTGGTTAAGATGGTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43 A T ---	---	CTCATAATTAGATTGAGATTGTGCAATTTGGCAAGAATATATG/A/TJTGATAACAATAATATGTCCTT ACTGGTGATATTAACCTTTGATACCTGGTTAAGATGGTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85 A C ---	---	ATTGTTTCCCTGAACATTCCTGGTGCTCCCTCTGAAAGCCGATGACCATCCAAACCCCTGGACTCACCT GAAATATCCTACGAGGC[A/C]TCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3693 a	30 C T ---	---	ATTGTTTCCCTGAACATTCCTGGTGCTCC[C]/TJCTGAAAGCCGATGACCATCCAAACCCCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3698 b	145 GA --?	---	TCCTGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCAAATCCCCAGGGTTGCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCCAAGGAATCCAGATTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51 C G ---	---	TCCTGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCAAATCCCCAGGGTTG[C/G]TCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCCAAGGAATCCAGATTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGAGAAATACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107 C T ---	---	ACCAGCCTCATGTGCAGAGGGTGCTCCTGCTGGATCCCAACTGGAGCCATCCCTGGGCCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104 GA ---	---	GCCAAACAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAATATATATTACCAGCCAAACAGCAACACAGCCC[G/A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAATAACGGCACATTTA
stSG3751	128 GA ---	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTCACTACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGATGTTCC[C/G/A]TT GCTGACTCCATGTGTTGCAAGAG
stSG3787	49 T A ---	---	TTCTGTGCAAAAGAAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTATTA/JAAAGTCCCTAAGA CACTGAGGGCATAAAACCAACAAATAAAATAAGGAGTAGAGCTAAAGCAGTATCTTCCCCT
stSG3880 b	115 GC ---	---	GACAAGAGGGGAAGAGATGCCCAAGAGACAGGGCTGGGGCAGCTGGGGTCCCTGAGTCCAGGGCCG CACCACACGTCCTGTGGTCAAGGCCCTCCTCTGGGGAGCAGGTCTA[G/C]GGCACGGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGGACCCAAAGAGTCCATTCTGCCCT

stSG3880 a	36 G C ---	---	GAC AAGAGGGAAGAGATGCGCCAGAGACCAGGGCTG/CJGGCAGCTGGGGTCCCTGAGTGCACGG CGCCACACACGTCCTGTGGGTCAAGGCCCTCCTCTGGGGAGCAGGCTAGGGCAGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCATTTCTGCCCT
stSG3895	44 A G ---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTTAGTGTG/A/GJTTTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATGGGAACAAGATGCTGATTCGTCACACTG AAAAT
stSG3902	104 T C ---	---	TCTGTTGAGACTGGAGAGACCAGGTACCAAGCACCGACTCTGGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTACCTAAATGTGAACCTGCTTTCTTTTC/T/CJTCAGCTCAATAGCTTAACATCTAAATTC ATGTTGCTCCCTTTGCTGGACAAT
stSG3935	50 G A ---	---	GGGTGCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCC/G/AJCTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACATATGGGGTCACAACCTTCTCGGACGT
stSG40	25 A G ---	---	GAGGAAGAGGTTGAAGAAGTGTGA/A/GJAAATATATTTAAGATTTCTTTGGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGATAAGGAACAAAATAAACCCCTTGTGTATGTATCA CCCAA
stSG4009	32 A G ---	---	GTGTGGGCTGTCTGATGATGAATGGCGGCTC/A/GJACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGGTTTTCCACACTGCTTACA
stSG4033	123 T C ---	---	AGAACCTTTGGGACAATGGCAGTGCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAACCTACAGTGCAGTAACCAAGAACCCTAATGTTTCAAGCATAAAGGTACTTT/CJGTGTAAC AGGTGGGCAACAC
stSG4038 a	29 G A ---	---	GCTGAGAGCACGTGTACAGCCACGCTGTG/AJCGCAGGCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTTACGGCTCCCGGAGAGCACCTGAGGGTTCCATCACT
stSG406	53 T C ---	---	ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAGCTAAACGAACAAAAT/CJGGTTTTAGTT TTGCTGAAGACTGGCCCTTATTATGGACAGCTTTCCCTAACAGAGATTATTAACCTTTTATCAGGTGTT AACATCTGTTTCAGGAACAIGGCA
stSG4095 b	55 G T ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAAGTACTATTGTCTGCTAGATGTATTAG/GTJATAAAAA GTTTGCCTCTGTAATACCTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCATTTGCCCTTCATCCTGG
stSG4095 a	27 A C ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTG/CJGATACTATTGTCTGCTAGATGTATTAGGATAAAAA GTTTGCCTCTGTAATACCTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCATTTGCCCTTCATCCTGG
stSG4120	65 G A ---	---	TGCATGTTCCACATCTTTTCATAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC/G/ AJCTTTTCCCTCAGAGAGCCCCACAGTTAAACACGTTCCAGCACACCATTAATCCACCGAGCT

stSG4128	54 A G ---	---	CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTTCT[A/G]TATATTATTT TACTTCTCTGAAATGCCACATAATTTGCAATAAATGATTCACTCCTTAGCTCCAAAAGCAAGTCC TTTATCAAAATGCAAATGTTCCAGAGGG
stSG4209 b	128 G A ---	---	CACGAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAAACATCCACATGGCACAAAGC AGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGGCGCGCACTCCCTC[G/A]GC AGGGGAACACCGAGGCGACAGGTGCTTTGATGCTCCGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65 G A ---	---	CACGAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAAACATCCACATGGCACAA[G /A]CAGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGGCGCGCACTCCCTCGGC AGGGGACCAACGGAGCGACAGGTGCTTTGATGCTCCGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31 G A ---	---	CATTACCCAGAACGCCATGGAGGACCAAGAGC[G/A]CCACGGCCGGGACTCCCGCGATGGCTGGGGGG GCTATGGCTCTGACAAAGGATGAGCGAGGGCGGGGGCTGCCTCTCCCCCAGGGGCGAGACGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCGGTCAATG
stSG4301	81 T G ---	---	TGCAACAGCTCTGAGAGGAAATCCTTTGGCAGATCAAAAGAGAGGGTAGTGGTCCACACATTTCCAT TTAAGCAATAAATTT[G]AGCTTCTGAGTAGTTGTTCCAGTTTACCCCAACATTTTG
stSG4331 b	71 T G ---	---	CTCACAAAGGCCAACACAGAAAAAGATACAAATACATTCACAGCTAATAATTTAGTTTTATGACAC AGAGT/GTTTTCAACAAGTTTAAAGTGTCACCTGAAGAGCATGTAAAAAGTTTAAAGTTATCACTT GGAGAGCAGATTCTTGGCCTCGCCCTTGATTTCTGTTTGGGGGTGTC
stSG4340	76 G A ---	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGAGATAACAATGTGTACACCTGGACCTGGAGAGCAGAA
stSG4361 b	109 A C ---	---	TTCCCAACCATTTGAGTGACAGAGCTC[C]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGG AAGTTCTTGGAAATTTCCATAAGGGATAACTGCATCTTTTGACCTTCACAACCTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4361 a	24 T C ---	---	TTCCCAACCATTTGAGTGACAGAGCTC[C]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGG CACAAGTTCTTGGAAATTTCCATAAGGGATAACTGCATCTTTTGACCTTCACAACCTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4376	73 A G ---	---	TTTCACTGCTACTGGTTTCGGTGTCTGAGTCCCTCAAACTCTGCTTTGCAAGTGCTTCTCCAAGGGGAG AACAGT/GCTGGAACCTGGGCTCTGCAGAAAGCCATCTTTCCAAAGCCATTTCTTCAGCTGC
stSG4381	50 T C ---	---	GAAGGCCACAACACTCCATAGCCAGAGAAATGACAACATACGATTTCTTTT/CJTCAAGTCTTGTAGT ATCCACAGTAGTGTCTGTCCATGTACAAGTGTCTGTCCAGAACACCCATTAATTCATGCC
stSG4410	79 A G ---	---	ACCAATGGTTCTGCTATGTGCATCCGATATTTTGGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAACACCCG[G]GTGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGGGGTGGCTTGT CAGCTGGGT

stSG443	65	C T	---	AGCAGATCAGTCAGCCACCTTGCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/
stSG4430				TJGTATGCAATGAGAAAATAACCAACTGGTAGGATGGGGAGGGAGGCAATAGGCAC
a	54	A G	---	AAATGGAATTCATCTCGCTGCTCTCTCAGGTC
stSG4448	99	G A	---	ATGCACATTAAATGAATGGCCTAACTACTGGGAACCTTTAGTAGTCTTATAAGGTJ/A/JATTAACATA
				GGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATAGGCATCAAGAGGGCCATTTT
stSG4448	99	G A	---	CCTCCCTCCCTCTCTCCCTTCACGCTTTCCATACTGTTCCCTCCCGCCCCACCCAGGCTCT
				CGCTAGCCCTGCCCTCTGGGTCACCTGC/G/JTGGGTTAGGCCCCCCAAAAA
stSG4449	92	T C	---	ATTAGCCATTTCATCTTGCAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT
				TAACTTTGGACAACCTTAAAACCTTA/J/C/JTAGTGACATTGCTGTCTAATAATCAAATACTTTCATCATA
				GGCTGAACATAATTATTAAAAGAGCAAAAGTTACCCCTCCC
stSG4467	42	C A	---	CAGACATGAGGGATGGCCCTGTCTCTCTGGGACAGAGCCCTCA/CJAGATGATGTCCATGTTTGTGT
				GAATGAACTCAAACACTCTTCAGTTTTTAGAGTCATTTTCTGGTATCGAGCGACACACCGGAG
stSG4475	21	A C	---	CACACCTGCTTCCAAGCTGCTGCCCTCTGACACAGT
				ACATGTCAATTCCTGACCAGGJ/C/JATTAATAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGGA
stSG4477	32	A G	---	TTAAGAGACACAAACTGGACTTTTGTCTTTCTTTACTGTAGCACCCAGGTTTCATG
				GTAACATTCCTGGGGTGGGGTGAGACAACA/JA/JATGAACCAATAATTAATTACAATTATACATT
				TCAAGGAGACTTTTAATCTAGGTTAATGTGAAACGACGCCATCAATGGTTGTCTAGGAAAAGGGAGA
stSG4531	79	C T	---	TGAAGCTTCTCTGGGGCAACGTTTGGCCTCATTGCAGTCAGACTTGGC
b	86	G A	---	TGAAGCTGAGGCTGGTGGGAGCTCGAGCGAGGGAGGCTGGGGGCGCAGATGAGCGCGCGGGA
a	85	C G	---	CAGCAGCGTCG/C/TGCCACGCTCTGGCGTTGGTAGAAGAGGACATAGGCTGCCCTGGACTCGATCT
stSG4550				GATTCATTGACAGGGGAGACGCTGTTGTCAATCA
stSG4550	86	G A	---	TGCATTAAGGAATGATACGGCATATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
stSG4550	85	C G	---	AAAAGAGACAGTGGGCACC/G/A/JCAATTTGGAGGGGAAGCGGGGCAAGGTTTATAGAGAAC
a	47	A G	---	TGCATTAAGGAATGATACGGCATATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
stSG4590	47	A G	---	AAAAGAGACAGTGGGCAC/C/G/JCAATTTGGAGGGGAAGCGGGGCAAGGTTTATAGAGAAC
				AATCAGGCACAAGCTCGGGAGAGAAGCCAAAGCTCTTCTGCA/JA/JATGGGAGGGAGACAC
				CATTGAAAAAGGCATCGTTCCTCTTCATGCAAGCGAGGCTGGCTCCACAGGCATGGTCTCCTTG
stSG4623	22	T C	---	AATCTGTATCACCCAGCGCTGGT/C/JCAATGTACTAGTAGCTTTCACAGGGATTTTTTATACTATTC
				CTATAAGGTTTTATCATGAATAAAAAGCTCACAACCTCTTTTCAGGCCATTGCAGATTTCACATTTATCT
				TAATATTCCTGTTCAAGATGCTCTGGAG
stSG4843	102	A C	---	TAAAAAAAACAACCCCCCAAAAAACACCCAGAAGTTTTTGTAGTTTTTATGTTTTCAGATTTTAAAG
				GTATTTCTTTCTAGCTTCTAAATTTTGTAGTCA/JA/JATCAGAAAAGTCTCCCTACTCCAAGGTGA
				GAAAGGA

stSG4850 a	38 C T ---	---	---	GGAACTCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC/TGTGCACTTGCAGGCCACGTCAGGAG AGCCAGCGGTGCTGCGGGAGGTTTCCAAAGGTGCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCC
stSG4879	86 A G ---	---	---	AACTCTGAAGGGGGTGACCTCAACCCAGCCCTGTCTTCTGTGAGGTCCTGCTTTTGCAGAAATGGCCTG CCCCTGGGACTGGAGCAG/G/C/TTGGGTGAGCTCTAGGTGGAGGGTGTGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104 G A ---	---	---	ACTGGACTGGCTGCTGCTGAGCCGGCTGAGCGGCTGAGCGGCTGGGACTGCGGCTGACCACTCGCTCTTCAG AGACTGCCCCCGGTGACCACTGACCTACGCTCTGCC/G/A/GTGGGAAAGCAGAAAGCAGGACC
stSG4896	112 C T ---	---	---	AAACAAATCAACCCAAATCCCAAGCAGTCTATGTACAGGCCACTCCCTGCTCTCTGCCATAGAGA GGTTGGGGGAGCTGAGGAGTGGTGGGGCTGGGCACCTTTTCT/C/T/CAGCCACAGGCCCCCTGAGG AATTAAATTGACTG
stSG4932	22 G A ---	---	---	ACAGTGCCGATGGTTACACAAATG/A/JTTGTAATGTATTTAAATCCCACTTACGAATGATTAAATGA TAAATCTTATGTTATTTTCATCACTACCAAAAGGCTGGGTGACGGGTGCTGGTTCTTGGTCTCT
stSG4950	24 A G ---	---	---	TCATGACTCCCAAGAAAGGTCTT/G/JCTTAGCTTCTCTCCCTACTTCTCTTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 G A ---	---	---	AGATACGGGCAAAACACTGGATGGCTTCCCTGACAACTTAAGAGGCTCCGAGTTATATCTGGGT GGGAAACACTGACCCAGCCCTTATTCCTTCAAGGACTCTAGTCATTGGCAAGGAGGATTCATGAGCC CC/G/A/GTGACACAGATGGGGCCCTGCTCTATATCAAC
stSG4961	91 C T ---	---	---	GAAGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAGGAAAGTA/C/TJAGAGAGGGCATTCAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 A G ---	---	---	ACTGGTGCTCTCAGCAGATTCAGGGGTGCTGAGGGCTGGTTACCACAACTCAGTAGGAGTGCAA GGGTJ/G/JTACCCCGGAGCTAGACAGCCTGGGTGAAATCTCAACTTCTCCCTTTTCTTGCTGTGC AACCTTG
stSG4997	22 T C ---	---	---	CAAAGGAGAGTAGGAGCCCCCAAT/C/JTTTAAATGGTTCTCTCCCTCATGCTATTTGATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGAGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAAT
stSG6312	37 C T ---	---	---	ACAGGTTCTCACACTTTGAGCCCTTAGTGCAAAAAC/A/C/JTTATGCCATGCGGGAAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATCTCAAGCAGAAGAC
stSG6345 a	107 G A ---	---	---	GCTCTGGTCAAGCAAAATCTCCAGGACAGAAGCAACAGGACAGTAACACACATGTATGACCCCTTA CAAGTGTCTTAAAGATTTTAAAAATGTGATGTTTGTCCAC/G/A/JATAGTTCAGGCAATTAAGAAAT GCAACCCAGAGAAATTTCTGTGAAAACATTTTGTCTTTTGGCCTGGTGTGGACAGAAAGGTGGCCAA ATGGATTGAGTGATGACGACATG

stSG6362	88 G C ---			---	TGTGAAATGTACACTCAGGCTAAACAAATACCTATTATTCTCTGGTTAAGAAAGGTTTAGCAGGAGCCTCCAATGAGCACTGTATGTAG/CJAGAAAAGGGAAGGAGCAGGAGGAGGAACACAGATCTGCACAGAAT
stSG8010	62 G T ---			---	CACATCTGTGTTTCTGGAGCAAAAGGGAAACCCACAGAAGGCCAGGAGTTTGGGTGTGCACCTGG[G/J]TGTCTTTCAACTGGGTGGAACCAAACTGAGTCTCTGAAGTCTCGCTCCCTGAGGCTGCAGAAGAATAGA
stSG8022	53 G A ---			---	AGCTCTGACTCCCTGTTACGTGACGTGATGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTTATTACACCATGGAACTGGAAACTCTACAAATCAATGCGTTTATTCTTTATTTTTCAGAGGGCAGGTTTATCAGCACACGCTGTATCTCC
stSG8032	67 G C ---			---	TGATTGTTAGGGATAAGTGGGCATTGTGTTTACAAATTAACCTCCAAAGAAATTCAGAAAATTTGTGTGTG/CJTGAGGAGCAGGGTAGCAAGATAAAAGAGGGAGGACAGCTGGGGTTGGTAAAA
stSG8064	46 C A ---			---	AGCTGGCTCTTCCTTCTGTCGGTTCGGGAGGCTTCACGTCTCG[C/A]CCGTGGTCCCTGGGTGGCCGAGGACCAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAAAACAGGGAACA
stSG8064	23 G C ---			---	AGCTGGCTCTTCCTTCTGTCGGT[G/C]TTCGGGAGGCTTCACGTCTCGCCGTGGTCCCTGGGTGGCCGAGGACCAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAAAACAGGGAACA
stSG8072	59 A G ---			---	CACCATCATCATCGAGTAGGCTGAGGAGCAGGAGGGGTGGGTCTTGCTGTCTTAGGG[G/A]GTGGCAGAGGCAGAAGGAGTCCGAGTATTAGTGGCCGCATGCAGTTCAGGCCTGTGCTGTTCAAAA
stSG8100	40 A G ---			---	ATACACCCACACACCCCACTCAACCTTGATCAAAATCCCA[G/A]GAGTGTAACTAAAGTATAAGAATATCATGACTAGTTAAAGATAGCAAAATACCAATAAGGTACAAGTTCAAGTATTAGTATAACCAAGTATCTGAGTAACAAATGTCTTGGAATGGG
stSG8102	138 T C ---			---	AAGGCTCCTTTGAAAGCATGGTTATTGTTCCATTTAACTGTCTCAGCTATACTGAAGTATGATTGACAAATAAACTTGCATATATTTGAGATGTACAGTGTGATGATACATGTATGTATACAAATGTGAAA
stSG8105	110 A G ---			---	TGA[T/C]TGTCTAATCATAATCAATAATTTGGTATATIGGTTAGGAATGTGATGGTCAGTGGTCTCAAACTCCAGCTACACGAGGATGGTCTTGCTTGTTAATACACAGATGACTAGGCC
stSG8130	96 T C ---			---	CACCTGCGGAGTTCCCTGTGGAGTCTAGGCCCTAGGCCTGAGAATATTC[G/J]TTCTAACAAGTTCCCAAGTTCCAGGTGACCTGAGGCTCTGGACTGGGGAACATGCTTTGAG
stSG8130	36 C G ---			---	GTGTGTACATCATTTGGGAATGGAGGGAATAAATGACTGGATGGTGGCTGCTTTTAAAGTTTCAAAATGACATCCAGACAAGCGGTGCCTGAGCC[T/C]GTGGCTGTCTCAGATCTTCACAGCACAGTTCC
stSG8145	124 T A ---			---	GTGTGTACATCATTTGGGAATGGAGGGAATAAATGAC[G/J]GGATGGTGGCTGCTTTTAAAGTTTCAAAATGACATTTCCAGACAAGCGGTGCCTGAGCCCTGTGCTGTCTTCAGATCTTCACAGCACAGTTCC
				---	TTGTGGACTTCAAATCTTTCCCTTCAGATTTTAAATGACATTTATGCATGTACATATTTTAAAAATTTAGACACATTTTAGAGAACACAATTTGTGAACACAAATCTAAGAAATGAATGAGATGT[T/A]CTGAAA
				---	TCTGATTCAAACACTTATCTTAACTGACTTCTGTCAATCTCTGCTGCTGTAAGG



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stSG8145 a	97	C T	---	---	TTGTGGACTTCAAATCTTCTCAGATTTTAAATGACATTATGCATGTACATATTTTAAATTT AGACACATTTTAGAGAACACAAATTGTGAAC/C/JACAAATCTAAGAAATGAATGAGATGTTCTGA TCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCTCTGCTCTGTGAAGG
stSG8150	36	A G	---	---	ATTGTTCTTGCAATTGCTTGGATTTTTCAGAATAGTJ/JGJATAAATAAACGGGAATCCTTAGGCAT TCGTGTTTTTCTATGTTTTAACAGGATTTTCTCTAATGTTTCGCTATTAAATACCATGCAGGAAAT GGGAAAT
stSG8340	30	C T	---	---	AGAGGATTATGGAGAGAGCTGGCAGGATC/JCAACATTATGACCCCTGAACCTCCAGAACCTGGAT TCACTAGAGGAGAGAGAGAAAACGCTCATCAAAA
stSG8466	111	G A	---	---	TGTGATTGGGTGACTGTAGCCTAAGGATAAATAAATGACAGCAATGTTATAAGCAGTGGGA GGAGTGAACCTGGGAATACCTGGTTACAAGGTAATTTGCACACTACCTJ/G/AJGGAAGCAGCACAGCATTAT TTGAAAG
ESTD-ACE	--	--	---	---	GATCAAGCAGTGCACACGGGTACGATGGACCAAGCTCTCCACAGTGCACCATGAGATGGCCATATA CAGTACTACTGCAGTACAAGGATCTGCCCGTCTCCCTGGTGGGGGGCCAAAGCCCGGCTCCATGA GGCCATTGGGGACGTGCTGGCGCTCTGGTCTCCACTCTGAACATCTGCACAAAATCGGCGTGC
ESTD-ADA	--	--	---	---	ACCATCTTATACTATGGCAGGTAAAGTCCATACAGAAGAGCCCTCTCCCTGGGATTTGAGTGGGTG CCAGCTCCACCCAGAGCCCTGGGGAATCCAGGGTCACTGTTCTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTGCAGACCC GCAGACCAACTCTGAGCTTCTGGGCCCTGAGTCTTGCTCTC
ESTD-AK- 168	--	--	---	---	GGGAGTGACAGCTAGAGCACCAAGGGGGCTCTACAGCTGTGTCTCATGGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	--	--	---	---	AATCCAGCACTTTAGGAGGCTGAGGCAGGCATATCACCAGAGTCAAGGATTTGAGACCAGTCTGA CCAACATGGTGAACCCCATCTCTACTATAAAATACAAAATAGCCAGGCATGGTGGTGCATGCCCTGT AATCCAGGAGGCTGAGGCAGGAGATCGCTTGAACCTGGAGGCGAAGGTTGTGGTGAGCCGAGAT GGCACCATTTGCACCTCCAGCCTGGGCAACAAAGAGTAAACTCTGTCTTC
ESTD- ANT1	--	--	---	---	TCTCTGTCTACTCTACTCCATTAGTTCAAGGTCAAGTGAAGAACTGGGGCAATTAACCAAGTAATCA TGGACTGCCCAACTGCCAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTACCTT TTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD- APOA2	--	--	---	---	CCAGGTGTTGTGGCACGTGCTGTATCCAGTACTCGGGAGACTGAGGCATGAGAATCTTTTGAAC CGGGAGGCGGAGGTTGCAGTGAGCTGACATCGCCCACTGCACCTCCAGCCTAGGTGACAGAGCAAG ACTCC
ESTD- APB8	--	--	---	---	GGAAAGAAATGGAGCCTGTGGGAAGGAGCGCTCCGAGGGGTGGGCTTTGTGGCAAGCCCCCTTGCCTGA AGCAGAAGGGCGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGGGAAACCATCAGTGAA GGAAGCCCATCCCCCAGAAATTGAGCTGCTGCATAATATTGACCCCAAC

ESTD-AT3a	--	--	---	---	---	AGACCTCAGTTTCTCTGTAAAGGGAAGTTTGTCTTGGATCTCCATGGGCCAGCCAGCACTG GTGCCCTGTGAGTCTGTATCAGGTAGAGAGATGGACACAGGTGGAGAGAAATTTGAAAGGGCATTG GAATTCAGAGCAAGAGACAGATATTAAGAGCTGGGAAATGTGG
ESTD-B3AR	--	--	---	---	---	GGCTGCCAGGGTTCCGTGGGAGCGGCCCTAGCCGGGCCCTGCTGGCGCTGGCGTGTGCTGGCCACC GTGGAGGCCAACCTGCTGTTGTCATCGTGGCCATCGCCCGGACTCCGAGACTCCAGACCATGACCAACGT GTTCTGACTTCGCTGGCGCAGCCGACCTGGTGATGGGACTCCTGGTGGTCCCGCGCGGCCCACTT GGCGC
ESTD-BA511	--	--	---	---	---	GGGCAACATAGTGAACCCCATCTCTACAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCCAGCTACTTGGGAGCTGAAGTGGGAGGATCCCTTAAGCCCTGGGAGGTGGAGGCTGCAG TGAGCCAAGATGGTGCCACTGCA
ESTD-BCL2	--	--	---	---	---	AGCTGGATTAACTCCTCTTCTTCTGGGGCCGTGGGGTGGAGCTGGGCGGAGAGGTGCCGTT GGCCCCGTGCTTTCTCTGGGAAGGATGGCGACGCTGGGAGAACAGGGTACGACAACCGGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTGCGAGAGGGCTACGAGTGGGATCGCGGAGATGTGG GGCGCGCCCCGGGGGCGCGCCCGGCACTCTCTCTCTCGCA
ESTD-BCR	--	--	---	---	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCATCTGCGCAAGA GACCAAGAGGTGAGCTTCTGTTGCCGGAAAGGAGGAGGAGGTGACAAGCTAACTCTGCTTCAAA ATCAACCATCCGGTGGACACTGTGTGGTCCCATCTGCCCTGGCACA
ESTD-BRCA1a	--	--	---	---	---	AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCCAAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCCAAAAACAGAA CCAAATAAAT
ESTD-BRCA1b	--	--	---	---	---	ACTAAATGAAGAAAAATCTGTAGAGAGGAAAACTTTGAGGAACATTCATATGTCACTGAAAGAGAA ATGGAAATGAGAACATTCGAAGTACAGTAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAGAACCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTA TTAATGAAA
ESTD-BRCA1c	--	--	---	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTGTCTGAAATGACATTAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAAAGA AATTAGAGTCTCTCAGAAGAGAACTTATCTAGTGGGATGAAGAGCTTCCC
ESTD-C1R	--	--	---	---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCTCTCTCCCTAATTTGCTCCGGGAAGCACATTTCATCAA
ESTD-C6	--	--	---	---	---	CCCAGTCAGTTTGGGGACAGCCATGCACCTGAGCCTCTGTTAGCCTTTCAACCCATGCATTCCATCTAA GCTCTGCAAAAT

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ESTD-C7	--	--	--	--	---	---	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	--	--	--	--	---	---	---	---	GGCAAGTTTTTATTGATAGAGAGGAATCAAATATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGCCAACCCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGGTGAACCATCAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCTAG TAACATAATTGTCTTCATTATGGTCTTTCCCGGCCTTCTCTCACACAC
ESTD-CB23	--	--	--	--	---	---	---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTTCCCGGCCTTCTCTCACACATACAGAGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCCTAGCCCATACCTCTTCCCTTCCAGAGGACCTGAAAACGCTGTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD-CB24	--	--	--	--	---	---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACACCCGAGGTGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCCGACACCGTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGACACAGACACCCGAGCCCTCAAGGAG
ESTD-CB25	--	--	--	--	---	---	---	---	GTTTTCTTCAGACTGTGGCTTCACTCCGCTAGTGAGTCTCTCTTTCTCTCTATCTTCGCCGTG TCTGCTCTGAAACCCAGGCGATGGAGATCCACGGACACAGGGCGTGAGGAGCCAGACCCCTG TGCACAGTACCTACATGCTCTGTTCTTGTCACAGAGCTTACCAGCAAGGGTCTGCTGCCACC ATCCTCTATGAGATCTGTAGGGAAGGCCACCTTGATGCCGTG
ESTD-CB27	--	--	--	--	---	---	---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTTGGGCTGGTTGCATTTCAAGAGTGTCTGTGGAGTCTGCTCATCACTGACCTATCTCTGA TTTAGGAAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTTCTCTCCACCCCAATGCTGCT TTCTCCTGTTTCATCCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD-COL2A1c	--	--	--	--	---	---	---	---	AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTTCCGTGACATTCAGGGTGTCAAGGTGGAAAAGGT GAACAGGTCCTCGTGGTCTCCAGGCTTCCAGTAACTCAAGCATATACAATACTGCTGCTTTG GTCAGCCTATTGAGCTGTAATCACCATACCCGTACCT
ESTD-COL2A1d	--	--	--	--	---	---	---	---	TGAGAGAACACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGACCTGGAACACTGGACTTCTTCTACTGCAGCAGACAAGACTTACCC AAGAGAGATTAAATGGCAAGATATACAATAACAATTTTATTGACCAAAACACTATCATGGAACAGC ATT
ESTD-CPT2	--	--	--	--	---	---	---	---	GCCGCAATGCCCGGAGTTTCTCCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGTATGCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGAGATGAAAAGCTACCATCACTCTCTCATCATGAAAAC TGGGAGGCCGGCATAGTGTCTCATGCTGTAATCCAGCATTTTGAGAGGCTGAGCGGGTGGATCAC TTGAGGTGAGGAGTTTGAGACCAACCTTGGCCAAACAT

ESTD- CTLA-4	--	--	--	---	---	ATGGCTTGCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCTACCAGGACCTGGCCCTGCAC TCTCCTGTTTTTCTTCTTTCATCCCTGCTTCTGCAAGCAATGACGCTGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGCATGCCAGCTTTGTGTGTGATGCATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	CAGGCCAGCGTGGTGAGGTGGTCAACCATCCCGGAGAGCAACAGGTGAGCCACCTATGCACAGGT TCTCATCAITGAAGCTGCTCTCAGGGTTCCCTTGGCCTGAGCAGGCGGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	AAAAAACATTTAACACCTTTTCAATCATATACACCATAAATTTCCATTTCACATAAGTCAGTT TGAGCTGAGTTTTCCAAATTACTTGCAATCTAAATGTCATACTGATTAAATGCAAGTTCAACAGACA ACTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCATAT CTGCATGTC
ESTD- D17S33	--	--	--	---	---	CATCCCCAAGCCCATCCTTAGCCACTGGCATTTTTTCCCGCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCCCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCGGTG GGGTTGTGTGGCTATGTGGTGGTCTTGTGTAGACGGGGCTTTGGTTTCAGTTGCACTATTGCGTTATT GCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCCTC
ESTD- D18S8	--	--	--	---	---	TTTGAGACCACCTGGCCAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGGTAGATGCCTATCGTAATCCAGCTACATCGGGAGGCTGAGCAGGAGAATTGCTTGAACCCA GGAGGCAGAGCTTGAGTGAGCCCAAGATCACACCACTGCACCTTACAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD- D3S11	--	--	--	---	---	AACTGATTAGAACCCTGAAAAATACATATTTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTTCATCATTAATAAAAAATCCAATAAAGTACACTGTAATAAAGAAATTAACAGAAATATCATTTGT TTATTCAAACTATTTATCACCTATTTTATTGGTAAGCCATACATAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	AGGTTCCACATTATTGCTGATGTTTGGTGGTTCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTGTTATTAAATTCAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCCTGC TGAGTCTTATTCAAAAACCTGACAGOCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTCCOC AGAAGTGAAACATACCTGCTCCTAGAACCCAGAGTCATCTGGATGTTCTGTTCCGGTCTTCACGATGG CAGGTATGAAATATAATATCTGTCTCTTTATTGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	--	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAAATGATTTT CTTAAACAATAAACTTGAAAGTCCAAAATTACTCCTTGATCCATGGACTGCAGAAATAAATGTTATTT TAGCTGTCAGAAAAACAATACTAATCTTGCAATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGATT GCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTTTCAATGCAGTAG
ESTD- D4S95	--	--	--	---	---	CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAAATTTGAGAAAGAGCAAAACAACCTTCAAGG ATAATGGGGCAATCACTTCTCTTCTCTTTAGAGTCAACCGG

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ESTD- D7S399	--	--	---	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCTCTTACAAACATTTTCATCCATGGACTCCATACCTAG AATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DM	--	--	---	---	---	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACGTGTGGCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCTGGGAGAGGAGGAGGGAGTGGGAGGGAGACA GAATGCTGATTATCTGTGGAGAACAGAACTTCTGGCCTGTGGTAGGGGAGCTGCTTCCAAGACC TCCTGATTGAGGAAGGGAGCAGCAGAGCGAAGAGAAGAGT
ESTD- DRD1	--	--	---	---	---	TCCCCAGCCTATCGGTCTATTTGGACTATGACACTGACGTCTCTCTGGAGAAAGATCCAAACCCATCAC ACAAAACGGTCAGACACCAACCTGAACCTGCAGATGAATCTGTCCACACATGCTCATCCCCAAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	--	--	---	---	---	TCTGCCTTTGGTCAGGAGGCTGCCGGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCGGTACAGCCCCATCCACCCAGCCACCCAGCTGACTCTCCCCGACCCG TCCCACACGGTCTCCACAGCACTCCGACAGCCCCGCCAACCAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	---	---	---	AAGACGATGGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGCATGTGGGGGGCGCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAAGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGGTGCGTGATGCCAAGGGCTTCTCTGTGAGGAGA
ESTD- ERB82	--	--	---	---	---	TCTTCAGGATCCGCATCTGCGCTGTTGGGCATCGCTCCGCTAGGTGTAGCGGCTCCACCAGCTGG GGTGAGGGGTGGTGGTCAAGTCCGGGGCGGTGCAGACCCACCGGGCTGGGAGGACTTCACCC CGCCTCACCTCCGTTTCTGCAGCAGTCTCCGCATCGTGTACT
ESTD- ETS2	--	--	---	---	---	ACTCAGAGTGTCTTTAAGTGAAATGGTCGAGAAAGAGCACCAGAGCCGCTGCTGGCGCTGGCA GTCCGTGGACGGGATGTTCTGGCTGTTTGAGATTTCAAAGGAGCGAGCATGTCTGGACACACAC AGACTATTTTAGATTTCTTTTGCCTTTTGCAACCCAGGAACAGCAAAATGCAAAAACCTCTTTGAGAGG GTAGGAGGGTGGGAAGGAACAACCATGTCTATTTTCAGAAAGTTTGTG
ESTD-F2	--	--	---	---	---	GATAAGTACACTGAGGCCCCAGGAGGTATTGCCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAAAGGCCGTAGGGGAACTGGGGGATCTAGGGGATGGGTAGGAATGGCCC AGCCAGTCCCGGGCGGTGCTGGTCCCAACAGAGGAGGCGCTGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	---	---	---	AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATTTGTGTAAGATGATGTTTAAAGTCAAACTTCATTTTTTTTCCATA GGTATGTCCTCAATTTATCCAGCACAAATTTGTTAAACAAAAAAC

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ESTD- GODH	--	--	---	---	---	CGCAGACCGGTGCTAGTGGGGTGGGAGTGTGGAGGAAGGAGGAGGAACTGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTCTTGCAAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGGACCTCTGGTGGCAACCGTGTCTGCTGCCCTGTTGAGCTGTCTGTCTGCGCAGTCGA CTCTGTCCCGAAATCCGAGAGCT
ESTD-GCK	--	--	---	---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTACGCCCTGCTGAGGCCACTCCTGGTCAACATGAC AACCACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGATCCCCACCCACACCTGGCTGG AGCAGGAAATGCCGAGCGGCCCTGAGCCCCAGGGAAGAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAAITTACTCAAAGCTGTCCCCAGGTACAG
ESTD- GNAT2	--	--	---	---	---	GACCCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCCACAGGCATATTG AAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTCCCTAGG
ESTD- GPPK2L	--	--	---	---	---	AGTCTCATCTGCGGTGTCAGGTAGATCCCTTTCACCGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	---	---	---	CTGGGCTCGCCGACAGCTGTGCACTGCACTGGAGCGGGCGGCGCAGGCTACCTCTATAGTGGGTGG TATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	---	---	---	TTGGAAGTTCTCCACTGTTAACCAGTCTATGTTGGCAATGTGGCTGGGCCACATCTGGCCTTG AGGCCCTGCAGGACCCCAAGAGGCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCTCACCAAGCTATGATAACCTTAATTACACCTTGAGCAAGAGTTCCGGCTCCGGCTTGATTCC AGATGGAGCTTTCCTTATCCCTGATGTTGGATTGGCTTCCCTGCTG
ESTD-HT2	--	--	---	---	---	GGGCTAAATTTCCGAGCACTTTGCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAGAGTGTGTACAGTTTGTACAGAGATAAAAGGATAACCTGGGGTTTTCTGTGC TTTGCTTCTTACATCCCTGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTCTGTGAAGTTTTCAAACAACACACACCTT
ESTD-HT4	--	--	---	---	---	ACCAACGAGCCCGGATACAGACACTCTTAAGTTTGGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTCTTGGTGCTTCTATCGGCAAGAATGCGTACTTATTTGAATAGTAGAGGTAA ACCACACGCCCAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGGCGTGAACCCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	---	---	---	AACACACAAGCCCCAGCGAGAATTGAACCTCGGACCCCTGGTTTACAAAGACAGTGCCTTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTGGTTTTCTTCCCTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTAGCTTGAGTAAATTCAGGATATTCCTCTACAAAATGAAA ACATTTTCGTGCTGTAAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	--	---	---	---	ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGGTGCCCTGGGAGAAGAAGGAGATGTTTC CAGGGCACACATAGCTTAGTGGAGACTC

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ESTD- IGHV4-6	--	--	--	---	---	TTTACTATTCAATGGATACAGAATTGTGGGAGTCACTATATCTCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTCCTACATTTGTGTGAGTGACGGGAGTGGTGAGTCGAGAGTGGTGGG TGACGGACATAATGATTCAGAAAAGCAATATGGAAGATGAGTATCTATGATACGAACTGAAAGT ATGTAATACATTCACAAAATACTAATAAACGGAGTTGAATATAAACCCCA
ESTD-IL1A	--	--	--	---	---	CAAAAGTAAGCACCCCAATAATGTTAGCTATTACTATCAATATTATTATTATTATTATTTT AGATGGAGTCTGGCTCTGTCAACCCAGGCTGGAGTGGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CTCTCGGTTTCATGCCATTCTCTCGCTCAGCTCCGAGTCCGAGTGGGAATACAGGCCACCCGCCACT GTCCCGGCTAATTTTGTATTTTGTAGTAGACGGAGTTCACCGT
ESTD-IL1B	--	--	--	---	---	CCACTACAGATGGATAAATGGGTACAAATGAAGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTCTCTCGCTCAGGAGCTCTCTGTCAATTGCAGG
ESTD- KRT10	--	--	--	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTGAGTGTACCTTTTGGCAATATT AAAGGAAGAAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTAIGTAGCTCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8	--	--	--	---	---	ACCTCACCCCTCCCTTAGCCCGTGGGAGCAGGAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAATTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCATCTCTCCGCTCAGGTTTACCACGTCAACATTTGACACA
ESTD- LF79	--	--	--	---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATTTGAACCGTAGCAAACTGCATTGGTATTAGA AAAAATAAAAATTTCCAATATGATGCTGTGTATACCTGCTCTGCCATGCAGCATCATAGCCTGT GGGAACCAAGGAGGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	---	---	TACACACTTTCCTTAGCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCCAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	--	---	---	TGTCAGTGTCCCTAGGGGCACTCACCACCTCCAGCTTCTCAGCTCTGCGCTGTCTGCTGCGCTGCA AGGGTTTGTCTAATTCATCAATGCTCTCTCATCTTTAGCAGCTGTGGGTTTTTGTGTTGTTTC TTCTGTTTTGCTTAGTATCTGACTACTTTTAAATTATAAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTTATAAAAATTTTTCACCTG
ESTD-MCC	--	--	--	---	---	TTGTCCAGGAGTGTGCTGATGCTGCTGCCCTCCAGCTCTGTCCCTAGCCGAATTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCGGAA TCTCAGGAAGTCTCTGTCTTCCAAGGGTTTGGTCAAGTTGCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTCTCTGTTTAGCATGG
ESTD-NF1	--	--	--	---	---	ATTATCCAGATGAATTTACAAAACATATACCAGATCCCAACAGACTGATATGGCTGGT

ESTD- NFB1	..	--	---	---	---	AAATGGACTTGATATTGTACAAAAAAGTTTTATTTCTAAAAAAGAAAAAAGAGAAA AAATTTAAGGGTGACTTATATCCACACTGCACACTGCCTAGCCCAAAACGCTTATTGGTAGG ATCAGCCCTCATTTTGTGCTTTTGAACTTTTGTAGGGACGAGAAAGATCATTTGAAATTTCTGAG AAAATCTCTTTTAAACCTCACCTTTGTGGGTTTTTGGAGAAGGTTATCA
ESTD- NPPA	--	--	---	---	---	TGTCCCTAGGCCCCAGCCCTGCTTGTCCCTCCCTGGCTGTTATCTTCAGTACTGCAAGAGAACACAGAC AT
ESTD- NPAMP	--	--	---	---	---	GGAGGAGGAGGTGGGAGGGGGTCTGTCTGCTCCAGGTCCACAGACCAGAGAGGGGCTCAGTG TATCCCCACCCCCAATGTGGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD- NRAS	--	--	---	---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT GGGTTTTCTTTATGTAGGGTGATATTGGATACTTTTTTGTTGTGATTATATATTAGCAATTTGAGGG ACAAACAGATAGGCAGAAATGGGCTTGAATAGTTAGATGCTTATTTAACCTTGGCAATAGCATTCG ATTCCCTGTGGTTTTTAATAAAAT
ESTD-OTC	--	--	---	---	---	GTGACCTTCTCACTTTAAAAAATTTACCGGAGAGAAATTAATATATATGCTATGGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGGAGGATGTATAACA
ESTD-PAH1	--	--	---	---	---	GCCACACACCCACCCAGCACACCTCCAACTCAGCCAGCAAGGTGTTGACACAAGAGAGGCCC TCAGGGGACAGAGAGAGCTGTGGACAGCTGGGAGTCAAGCGTGATCATCGGAGGGCGGGGCAC ATGGAGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCAAGTCTTAGACAGACAAAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	--	--	---	---	---	CTCTTCAGGAACCAACCACTCTTACCAAAACACGACTTATGCTGTCGAGAGGTACAACCCGTAGA ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTCTTCACITTTCTGTTCTAGAACGTTTTCTAG GACTGGCAGTTTAAGCTTTCACCTTAGGCTTTCTGTATACCCCATGCC
ESTD- PBDA	--	--	---	---	---	CCTTCTCATGCCAGATGGAAATTCAGTCCCTTCAGGATCTGCCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGGAGGACTAATCCAAATCTCTACCCGAGCTTGTCTGCATACAGACG GACAGTGTGGTGGCAACATTGAAGCCCTCGTACC
ESTD-PS-1	--	--	---	---	---	GGGGAGTAAACTTGGATTGGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCCTCAGCAACA GCCAGTGGAGACTGGAACACACACCATAGCCTATTTCTAGCCATATTAATTTGGTTGTGCCCTTACATT ATTACTCTTGCCATTTTCAAGAAAGCATTTGCCAGCTCTCCAATCTCCATCACCTTTGGGCTTGT CTACTTTGCCACAGATTATCTGTA
ESTD- PXMP1	--	--	---	---	---	ATGAACATGGTTCTTTAATTTATGATATGTTTGTATAGCTATCTTAAAGGGCTCTCTTTTTTTA ATGCAGAAAGAGGGGAAAGAGCGAGCTGTGGTGACAAGGTGTTTTCTCAAGGCTCATACAGA TTCTGAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATTAATCTT
ESTD- Per/RDS	--	--	---	---	---	ACCTACAGACGTCGCTGGATGGTGTGTCACCCAGGAAATCTGAGAGCGAGAGCAGGGCTGGCTG CTGGAGAAGAGCGTCCCGAGACCTGGAAGGCT



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ESTD-RDS	--	--	--	---	---	CCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTGCTGGAGAAAGAGCGTCCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAGCTGGGCAAGGCAACAGGTGAAGCCGAGGGCGCAGACGCGAGG CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCAC CCAAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- PVR1	--	--	---	---	---	CTTCGTACGGGAGGTCACGTCTCCGCTCTTTCATGGACATATGGATGAGTGTGACCAATTCC CTGCTGACAGTATGACCGCAGACTTGTCTACTATGAGAGGGAGCTGTGTCACATCATGCCCGC TCCCTCTGGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGAGCCACCTGCCGTGGGGCCAGCCACT CCGAGTCGGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	---	---	---	TGAACACCTGTGGTCCGGAGCCAGGTGTGTTCTCTCGGGAGCCTGAGGAGTTGTGTCTGTGTG CAGTCCCGGCGCACCTGTCTGGTTGAGCCTGGACATACACCTTCACTCTTTGGCCGGAGAGAC ATTTACCCACCTGGCCATGTCCCTGGCTGTGTGACACACCTCTGTGAAGACCCCAACCCCTGCCTCC CCCACCAAGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	---	---	---	TTACATTTGTGGATTGTTCTTTTGTGTGTCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTTGGCTGCTGTGTGGGATATTTGAAGAGATCTTTGCCAGTCCATGTCTCTAGAGAG TTTTCCCAATGTTTCTGTAATAGTTTCATAGTTTGAGGCCCTAGATTTAAGTCTTTAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	--	--	---	---	---	AAATGGTCAGGACCCCTGATCCACAAGAAGTGGTACCATTTTCATCAGGGCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTACAACCTTTCTTCCAGTATGGATGGGATATGATGGGGGG GAGAAGCAAAATTTTAAATAGGACCCCATGAGACACATCA
ESTD- THR8	--	--	---	---	---	TGCGGCTTTCTCCGGCAGGGTAGACTTCTTACTGGCTGTTGATTTCCAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACAGGATCAGTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	---	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAGAAATGGAGG CAATAGGTTTGAGGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCCAGAAGACCCCTCAGAAATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGCCCAACTTTCCAAATCCCGCCCGCGGATGG
ESTD-TYR	--	--	---	---	---	TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGAATTTCTGTTCCACCGCAACAAGAGAGTCTATGC CAAGGCAGAAAGCTGTGCTTCATGGCAAAATCAATGTCTCTCCAGATTTCCAGATCCCAAGCA GTGCATCCATTGACACATAATAATGTCATCCAGACAAAGAGGTCAATAATATTGATGTCTGTTAAACAT GGGTGTTGATCCATTTTCATTTGGCCATAGGTCCCTATGGGGATGACA

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ESTD- TYRP1	--	--	--	---	---	AGTAGTGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATCTGATTTCTTTCACTTTATTACCTTCTTTCT AATACAAGCATATGTTAGAATTAAGTTCTAGGCATACCT
ESTD- VB12	--	--	--	---	---	TTCCCAAGCCTCAATACAAGCTTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACAAAGGTACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCACCCAGACTGAGAACCCACCGTTATATGTACTGGTATCGACAAGACCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	--	--	--	---	---	AGGTAGGAAAGCAAGAGATTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCTTTGG TCCCCTAGAGTCTG
ESTD-WT1	--	--	--	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTTACTCTCTGCTGCAGGATGTG CGACGTGTGCTGGAGTAGCCCCGACTCTGTACGGTCGGCATCTGAGACCAGTGAGAAACGCCCTT CATGTGTGCTTACCAGGCTGCAA
ESTD- s14544	--	--	--	---	---	TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCCTCAGTTCGCTGTGTGGGTTAGATGCAGGATTATATGATCOGTTAACC TCT
EST71770 6	--	--	--	---	---	AGCACCACTCTCACGTCAAGCCTCAGCACCATGCTGTCTATAAGGATGACGTGCTTTTACAA CATCTCCTCCATGAAGAGCACAGAGATTATTTATCTGAGTCCGGATCTATGACTCAGGGACAT ATAAATGTAAGTGTGTTGAACAACAAGAGAAACCCACTGCAGAGTACCAGCTGTTGGTGAAGG AGTGCCCAAGTCCCAGGGTGACACTGGACAAAGAAAGAGGCCATCCAAGG
EST32418 6	--	--	--	---	---	CAAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCAGTCAACCTTTGGTGGCTACAAGATGTG GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAAMGTGAACACTGTGAGTGTGG CCCACCTATTTGCCAGCCCGAGGGACAGAGCTGATCCTTGAACCTTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGCCAGGGCTGGCTTATCAGCTCCAGCCAGACCCCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGTAGAGACTGCGAGAAAGGAGGTGCGTCTGCTGCCTGCCCGG GTCACTC
EST13586 3	--	--	--	---	---	AGGCAGAAACTGGGCCCCCATGCGGGGGGACGTGGAAGGCCACTTGAGCTTCTCGGAGAAGGACCTGA GGGACAAGGTCAACTCCTTCTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGGAGGAGCAGCAGGAGGAGGAGGATGCTGGCC
EST51976 7	--	--	--	---	---	CCCTTGAGAGCTGAGCTGCCCCCTGGTGC

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EST11458 6	--	--	---	---	---	CCACITTTGGTAGTGCCAGTGTGACTCATCCACAATGATTCTCCAGTGTCTCATCTTGTTCGAGTTTCTCTGCCATGTTGCTATTGCAGGAGGACCTGTCCCAAGCCAGATGATTACCATTTCCACAGTGGTCCCATTAAAACATTCTATGAGCCAGGAGAGATTACGTATTCCTGCAAGCCGGCTATGTGTCCCGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	---	---	---	CGGCTCTCCCTCCAGGTATTGTGCAGAAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAGGCATTCTTGAGGTGAGTACACCTTCCCACTCTCTACGGTACAGAAAGGAGATGCATGAACAGCAGGAACACGTGGAAAGGCCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAATACAGCCCT
EST62448 0	--	--	---	---	---	ACCTGGTGTGCTGGTGTGCTGAGCTGAACCTGGTCTCTTGGCATTGCCGGCCCTCCTGGGCCCTGGTGGTCTCTCTGGTGTGCTGGTAGTCTGGAGTCAACGGTGTCTCTAGTGAAGCTGGTGTGATGGCAACCCTGGGAACGATGGTCCCCCAGGTGCGGATGGTCAACCCGGACACAAAGGAGCGCGGTTACCCCTGGCAATAT
EST36027 2	--	--	---	---	---	AGTGACTTCCAAGGAAATGGCTACCCCAACTTGCCTTCATGCGCTGTCTGGCCAACTATGCTCTCTCAGAACATCACCTACCACTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGGAAACCTGAAAAAGGCTGTCACTTACAGGGCTAATGATGTTGAACCTTGTCTGAGGGCAACAGCAGGTTCACTTACACTGTTCTGTAGATGGCTGCTCTAAAAAGACAATGAATGGGGAAGACAA
EST12274 0	--	--	---	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTCTTGGCTTCCAATAGAGCCTTACCAAAGTGTATTACATAAAGAAAGTCAAGTGGTTTACTCTCATGACCAATATCTTCCCTCTTAGGATGAGGTGATAGTAATGACCGATGGGTGAGAACTGTTCTGTCAACCATGGAGGATATACTAAGTGTGAAGATAAATTCAAGCCACAGAGCTTGCCAGATC
EST76807 7	--	--	---	---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCGATTGTCTCTATCTCCAGCGGCCCTGTGATCAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCACCACTGCCCCCTGCTGCCATGTGGACTGGTGCAGTTGAGGACTTCTTG
EST44438 3	--	--	---	---	---	GCAGCGAGGAGCCGCTGCACCATGCCCGCATAGATGCGGAACCTCAAGCTCGACTTCAAGGACGTCTGCTCCGACCTAAGCGGAGCGCTCAAGAGCCGAGCCGAGGTGG
EST12839 3	--	--	---	---	---	TGCAAAACACACAAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTCTTGTGCTTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAAGGCCATTGGCTATCTCAACACTGGTGAAGTACTTGAAGTAAAGGAACTTGAATGTTATTCAACTGGATTCCAGTAGGTTTCAGTTACTTATGAATATATGATACTTAGCTTAG
EST54419 8	--	--	---	---	---	CTTCTGCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCACTTTTATGGCACAATGATCACTATTTCTTGACCCCTACTTACAATCCTGGGAGATGTTATTTGGGTTTAGCGTGTGCTATGTTGCTACTATAGTCCAAGTGAA

EST10398 2	--	--	---	---	---	---	TGCTGGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTACATTTGGGGCTTGACTTTTCCAAACACGGAGAAG CATTTGTTCTTCGGGCAAGGATATCTACCAATAGTGTCTATTAGGCAATTG
EST36751 7	--	--	---	---	---	---	CCAAAGTCGTTCAATTTTAGCTTTCAGGTTTAACTCGATTACTTTTCTATTCAAAATCTCTGTAAAA TTGAAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST43562	--	--	---	---	---	---	CACGTGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGATCTGCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCATTATAACAAATATTTTACCTTTTGAAGAAATAAATG AAGGATTGACCTGCTTCGCTCTGGAAGAGATACCGTACCGTCTGACGTTTGAACAATACAGAT GCCTCCCTTGTAGCAGTTTTCAGCCCTCTACCCCTA
EST18288 3	--	--	---	---	---	---	GCCTCTATACCCCTGTGGTCTCTCCACGCTCTCTGGACTTCACAGAACCTGGATGTTGCTGCTGAGAA GATTGACAGGTTGATGACAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGACGGGAGCCAGTGTGG ACAGCACCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAGGCAACCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	--	--	---	---	---	---	TTCCCGCAGCCCCOATCTTGGCACCTGGTCCCTCTCAGGGGCCACCCGCGGGACTCACCGCTCT CGCTCTCGTGAACATCCGGCCGGCGCTCTTGAGCACATAGCTTGACCCGTTTCCGTATAGGAGG ACCGTGTAGGCCCTCTGTCCTCCGGCCCTTCCAGGGCCAGCCCTGCAGAGAGAGGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGTG
EST58707 7	--	--	---	---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTACATGAAGGCCAAATTCGAGAGAGCCCTAGAAGATACACGAGACCGA ATGTATCAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTGTGGTAGCCAGGTTTATAGCA CACTGTCAOCTACATTTCTGATTGGTGGACTCTTGTCTGAAGAACCTT
EST74167 6	--	--	---	---	---	---	AGACCATGAAGGAGTTGAAGCCCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGGAGCTGCAGGGCGGCAGCCCGGCTGGGCGGAGACATGGAGGA CGTCCGGCGCGCTGTGTGAGTACCGCGCGAGGTGCAGGCCATGCTGGCCAGAGCACCGAGGAGCG TGCGGGTGGCTCGCTCCACCTGGCAAGCTGCGTAAGCGGCTCCTC
EST43211 8	--	--	---	---	---	---	CGCTGTGTGCAGTACCGGGGAGGTGCAGGCCATGCTGGCCAGAGCACCGAGGAGCTGGGGTGGCG CCTCGCTCCACCTGGCAAGCTGCGTAAGCGGCTCTCCCGCATGCCGATGACCTGCAAGAAGCGCC TGGCAGTGTACAGGCGGGGCGCGAGGGCGCGAGCGCGCTCAGCGCATCCCGCGAGCGCTG GGGCGCTGGTGAACAGGGCGCGGTGGGGCGCGCACTGTGGGCTC
EST36770	--	--	---	---	---	---	TGTAGCCAAAGTCACCTGCATCATATTTGGCTGCTGGCAGGCTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTCTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGCTGGCCCTGACCAAAATATACTGGGTTTCTGTTCTCTTTCTGTATCAT TCTTACAAGTTATACTCTTATTTGGAAGGCCCTAAAGAAGGCTTATG

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EST26021 1	--	--	---	---	---	TAATGTAGCTCATCCACCAAGAAGCCTGCACCATGTTTGAGGTGAGTGACATGTTGAAACCTGT CCATAAAGTAATTTGTGAAAGAGGAGCAAGAGAACATTCTCTGACGACTTCACCTACCAATGA GCATTAGCTACTTTTCAGAAATGAAGGAGAAATGCAATTATGTGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTTTTGAACAAGACAAAGCAAAGCC
EST51212 0	--	--	---	---	---	ATCCTGAGCTCGCCAATAAGCTTCTTGTTCTACTCTCTCTCCACAAGCCCCAAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	--	--	---	---	---	GTCCGAATCTCTCTGAAAGTGCCGGGTTTAAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGCCTTGAAGCTGGAGTGGGTTTAGGGACCGGGTCTCTGCGTGCATCCTAAGCTCT GAGGCAAACTCTCTTGAAGCTGGAGTGGGTTTAGGGACCGGGTCTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	--	--	---	---	---	ACAATCCAGGTACACATTCCAGAAGAGGAGGGGTGGTGCAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	--	--	---	---	---	CTTCTATGGGATTGACTTTATTTCTCCATTGTCTTACCCTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGCAAGCTCATGACAAATTTGAAGCTGACAAATACACAAGAGGAAATAAATTCACAGTCAA AGAAATCAAGACTTTTCGAAACATTGAAGTTGTTTGAACCTGGTGTACACCTTTAATTACAACCTAG CAGACGGAACCTGAAGTCAAGGTAAGAAT
EST34088 2	--	--	---	---	---	GTGGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGGCCACAAAGAGAACCGGCTCAAGG ATCCCAAGGCCCACTCCCGAACCACTCAGGGTCCCTGTGGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	---	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCCCTTGGGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAGAGGACCCAGAAAT CACAGGTGGGCACGTGCGTCTACCGCCATCTCCCTCTCACGGGAATTTTCAGGGTAAACT
EST74082 --	--	--	---	---	---	TCCAGGGTGGCTGGACCCAGGCCCAAGCTCTGCAGCAGGAGGACGTGGCTGGCTCGTGAAGCATG TGGGGGTGAGCCAGGGGGCCCAAGGCAGGGCACCTGGCTTCAGCCTGCCTCAGCCCTGCCTGTCAC CCAGATCACTGTCTTCTGCCATGGCCCTGTGGATGCGCCTCTGCCCCCTGCTGGCGCTGCTGGCCCTC TGGGGACCTGACCCAGCCGAGCCCTTTGTGAACCAACACCTGTGGC
EST45311 0	--	--	---	---	---	GGCCTCCTCTCTCCAATTCTGTCCTTATAGTTTTCCTCTATTAAAGTGAACATACATGCTCTTTAGT GGATAGATGCACACAAACACACAAGCCATTATGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTTCATTTAACAGCCCTTATTCATGGCCCTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCAATTTGTTGAAT

EST65258 8	--	--	---	---	TGCCCCATACGGCGCGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAAACCAGAAAT CCAGTTATTTCCACCCTCAAATGACAGCCATGGCGCGGGTCTCTCGGGGCTCGCGGGGG ACAGCTCCACTCTGACTGCCACAGCTTTGCATGGAGACTTGAGGAGGGAGGCTTGAGGTTGGTGAG GTTAGGTGGTGTTCTCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	--	--	---	---	ATGCAGGATGAAGGTGACAGGGAGGAGAGGGCCAACTGTGATCCAGGGCCTGCAGATGTCGCTG GACTATGGGTTTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	--	--	---	---	ATACTAGTACAAGTGTAAATTTTGTACATTACACTAAATATTAGCAITTTGTTTAGCATTACCTAA TTTTTTTCTGCTCCATGCAGACTGTAGCTTTTAACTTAATGCTTAITTTTAAATGACAGTGAAG TTTTTTTTCTCGAAGTCCAGTATCCAGAGTTTTGGTTTTTGAAGTGAATGCCTGTGAAAAA GAACTGAATACCTAAGATTTCTGTCTGGGGTTTTTGGTGCATGCA
EST35879 9	--	--	---	---	GAGATCGGTGTGAGTATTAGGCATGGTTACCTGTGATTCGCCAATCTTGCGGTTCCACCGATG GAACTGCCGCAATCTGACACGTGTGACCCAGGCTGTACCCAATTAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGAA
EST68308 5	--	--	---	---	GGAAAGAGATTAAAGAAGCTTGATTGGACAATCTGGTCTTTGAGTGTGGAAGAGTTTATGCTCT GCTGAGTTACAACAGAAATCCTTTAGTACAGCGAGTAATAGATATATTGACACAGATGGGAATGGA GAAGTAGACTTTAAAGGTAAGAAAGTAGTTATTTTTA
EST54045 6	--	--	---	---	GGAAATATAAAAATATTTAAATACCTCCATTTGCTTATCCTTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATTGTGATGTGGCAATTTGTTCTTACAAAATCGGATGGGAAATCT GTTAAGTAAGTACTGTTTGCTTGGAAATGGATTTTAAATGTGACTTTATCAT
EST52908 0	--	--	---	---	ATCACAGGTCTGTGCTCTGGCCATCAITTCCTGGGAGAGATGGATGGTGGTCTGCAAGCCCTTGG CAATGIGAGATTGTATG
EST19590	--	--	---	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAATGAC
EST76136	--	--	---	---	TGAAGCTTCTGCCAGCTTGCAITTTCTAGGAGAACCCTGTCATACCTTTATCTATAGCCTTCCCC TAGGCTTT
EST58607 0	--	--	---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAAGGACAGCCACATGGCGGGATGGCGGGGAGTCTGGT TGCGGCCACGGCTGTGGCTCGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGTTCT TGCCCAAGGAGGGGGGGTGGCATGCCTGAGATGTAGATGCGGOC

Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer  
6=SNP Reverse Primer 7=Sequence

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## EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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## CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,  
or a portion thereof which includes a polymorphic site,  
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is  
biallelic.
8. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is the reference base  
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is an alternative form  
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a  
20 segment of a fragment shown in the Table, column 7 or  
its complement.
11. The allele-specific oligonucleotide of claim 10 that is  
a probe.



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12. The allele-specific oligonucleotide of claim 10,  
wherein a central position of the probe aligns with the  
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is  
5 a primer.
14. The allele-specific oligonucleotide of claim 13,  
wherein the 3' end of the primer aligns with the  
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which  
10 is selected from the group consisting of the nucleotide  
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which  
is selected from the group consisting of the nucleotide  
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the  
Table, column 7 or the complement thereof, wherein the  
polymorphic site within the sequence or complement is  
occupied by a base other than the reference base shown  
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising  
obtaining the nucleic acid from an individual; and  
determining a base occupying any one of the polymorphic  
sites shown in the Table.
19. The method of claim 18, wherein the determining  
25 comprises determining a set of bases occupying a set of  
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method  
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<b>(21) International Application Number:</b> PCT/US97/20313 <b>(22) International Filing Date:</b> 5 November 1997 (05.11.97)  <b>(30) Priority Data:</b> 60/030,455                      6 November 1996 (06.11.96)                      US  <b>(71) Applicant (for all designated States except US):</b> WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US).  <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Mass- achusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA).  <b>(74) Agents:</b> GRANAHAN, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).	<b>(81) Designated States:</b> JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).  <b>Published</b> <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims</i> <i>and to be republished in the event of the receipt of amendments.</i>  <b>(88) Date of publication of the international search report:</b> 12 November 1998 (12.11.98)	
<b>(54) Title:</b> BIALLELIC MARKERS  <b>(57) Abstract</b>  The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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## INTERNATIONAL SEARCH REPORT

International Application No

P S 97/20313

A. CLASSIFICATION OF SUBJECT MATTER  
IPC 6 C12Q1/68 C12N15/11

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)  
IPC 6 C12Q C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 12607 A (MOLECULAR TOOL INC) 11 May 1995 see the whole document ---	1-20
X	WANG D ET AL: "TOWARD A THIRD GENERATION GENETIC MAP OF THE HUMAN GENOME BASED ON BI-ALLELIC POLYMORPHISMS" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 59, no. 4, October 1996, page A03 XP002050641 see abstract --- -/--	1-20

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

## \* Special categories of cited documents:

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
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- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

- \*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- \*X\* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- \*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- \*Z\* document member of the same patent family

Date of the actual completion of the international search

17 June 1998

Date of mailing of the international search report

23. 09. 1998

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## INTERNATIONAL SEARCH REPORT

International Application No

PC

97/20313

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL10 embl Accession number: hst27766, 12 January 1995 ADAMS M D ET AL.: "Initial assessment of human gene diversity and expression patterns based upon 52 million basepairs of cDNA sequence" XP002067789 * Sequence *</p>	1-3,10, 11
X	<p>SYVANEN A -CH ET AL: "IDENTIFICATION OF INDIVIDUALS BY ANALYSIS OF BIALLELIC DNA MARKERS, USING PCR AND SOLID-PHASE MINISEQUENCING" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 52, no. 1, January 1993, pages 46-59, XP002050638 see abstract see page 47, column 1, paragraph 3 - page 50, column 1, paragraph 1 see page 51, column 1, paragraph 3; figure 1; table 1</p>	1-3, 7-10,13, 14,17-20
X	<p>FR 2 722 295 A (ROUSSY INST GUSTAVE) 12 January 1996 see abstract see page 1, line 5 - page 2, line 17 see page 9, line 9 - page 10, line 15; tables 2,3</p>	1-3,7-9, 17-20
X	<p>HRUBAN R H ET AL: "K-RAS ONCOGENE ACTIVATION IN ADENOCARCINOMA OF THE HUMAN PANCREAS A STUDY OF 82 CARCINOMAS USING A COMBINATION OF MUTANT-ENRICHED POLYMERASE CHAIN REACTION ANALYSIS AND ALLELE-SPECIFIC OLIGONUCLEOTIDE HYBRIDIZATION" AMERICAN JOURNAL OF PATHOLOGY, vol. 143, no. 2, 1 August 1993, pages 545-554, XP000572114 see the whole document</p>	10-16, 18-20
X	<p>GROMPE M: "THE RAPID DETECTION OF UNKNOWN MUTATIONS IN NUCLEIC ACIDS" NATURE GENETICS, vol. 5, no. 2, October 1993, pages 111-117, XP000615290 see the whole document</p>	18-20

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# INTERNATIONAL SEARCH REPORT

International Application No  
US 97/20313

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>NIKIFOROV T T ET AL: "GENETIC BIT ANALYSIS: A SOLID PHASE METHOD FOR TYPING SINGLE NUCLEOTIDE POLYMORPHISMS" NUCLEIC ACIDS RESEARCH, vol. 22, no. 20, October 1994, pages 4167-4175, XP002015765 see the whole document</p> <p>-----</p>	18-20

# INTERNATIONAL SEARCH REPORT

I. International application No.  
PCT/US 97/20313

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
  
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
  
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
  
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
  
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-20 (partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.



FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-20 (partially)

INVENTION 1: An isolated nucleic acid segment including a polymorphic site having the nucleotide sequence of SEQ ID NO:1149, or the complement of that segment or portions thereof, an allele-specific oligonucleotide probe or primer hybridizing to such a segment or its complement, and a method of analyzing such a nucleic acid by determining the bases occupying the polymorphic site(s).

2. Claims: 1-20 (partially)

INVENTION 2 to INVENTION 2669:

-Idem as invention 1 but limited to the sequences having SEQ ID Nos. 1150 to 3817. (Invention 2 is limited to SEQ ID NO:1150, invention 3 is limited to SEQ ID NO:1151, ..., invention 2269 is limited to SEQ ID NO:3817).

For the sake of conciseness, the first group is explicitly defined, the other groups are defined by analogy hereto.

# INTERNATIONAL SEARCH REPORT

..Or.. in patent family members

International Application No

F S 97/20313

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9512607 A	11-05-95	AU 8132194 A	23-05-95
		CA 2175695 A	11-05-95
		EP 0726905 A	21-08-96
		US 5762876 A	09-06-98
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FR 2722295 A	12-01-96	NONE	
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